

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 24, 2001, 17:32:30 ; Search time 32.57 Seconds  
(without alignments)  
787.349 Million cell updates/sec

Title: US-09-532-263-5

Perfect score: 2282

Sequence: 1 MSSCSGLSLVAVATLV.....KPGFLASVIPVDRRPGAPNL 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

al number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

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1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
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19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2282	100.0	423	17 AAR92814	Human interleukin-
2	2257.5	98.9	422	17 AAR99090	Human interleukin-
3	2257.5	98.9	422	22 AAB36654	Human IL-11 recept
4	1879.5	82.4	432	17 AAR92813	Murine interleukin
5	1853.5	81.2	432	22 AAB36653	Mouse IL-11 recept
6	1813.5	79.5	441	17 AAR99091	Murine Etl-2 gene
7	1662.5	72.9	379	21 AAR59390	Murine soluble int
8	402	17.6	460	13 AAR2616	IL-6R for soluble
9	402	17.6	460	22 AAB36656	Mouse IL-6 recepto
10	389	17.0	460	12 AAR13318	IL-6 receptor, Mu
11	370.5	16.2	468	17 AAR98364	Interleukin-6 rece

12	367.5	16.1	468	10 AAP90284	Sequence of a rece
13	367.5	16.1	468	14 AAR37215	IL-6 receptor. Sy
14	367.5	16.1	468	22 AAB36655	Human IL-6 recepto
15	366.5	16.1	372	13 AAR20024	Ciliary neurotroph
16	366.5	16.1	372	14 AAR37820	Sequence of human
17	366.5	16.1	372	16 AAR70147	Human recombinant
18	358.5	15.7	468	10 AAP90525	B cell stimulating
19	357.5	15.7	468	19 AAW71371	Human interleukin-
20	346.5	15.2	1158	21 AAY92205	Fusion polypeptide
21	343	15.0	525	18 AAW36846	Human fusion polyp
22	339.5	14.9	1168	21 AAY92204	Fusion polypeptide
23	338	14.8	543	20 AAY03164	Chimeric sIL-6R/IL
24	337.5	14.8	344	10 AAP90528	B cell stimulating
25	337.5	14.8	345	21 AAY55071	SRJ45 protein sequ
26	337	14.8	360	20 AAW70804	Amino acid sequenc
27	337	14.8	360	21 AAY92199	Soluble human IL-6
28	337	14.8	468	21 AAY92196	Human IL-6R-alpha-
29	337	14.8	477	21 AAY92197	Human IL-6R-alpha-
30	337	14.8	592	20 AAW70797	Human interleukin-
31	337	14.8	592	21 AAY92185	Human IL-6R-alpha-
32	337	14.8	690	21 AAY92195	Human IL-6R-alpha-
33	330	14.5	515	21 AAB15404	IL-6R/IL-6 fusion
34	328.5	14.4	323	10 AAP90527	B cell stimulating
35	324	14.2	1042	16 AAR70122	IL8-R type 1-GBP 1
36	323.5	14.2	325	21 AAB15389	Human interleukin
37	323.5	14.2	325	21 AAB15390	Bovine interleukin
38	322.5	14.1	315	20 AAW70805	Amino acid sequenc
39	322.5	14.1	315	21 AAY92200	Soluble human IL-6
40	307.5	13.5	326	15 AAR58304	Rat ciliary neutro
41	307.5	13.5	500	18 AAW36847	Human fusion polyp
42	261.5	11.5	228	22 AAB36651	Mouse cytokine rec
43	247	10.8	229	18 AAW09779	Epstein barr virus
44	244	10.7	229	19 AAW53624	Epstein barr virus
45	244	10.7	229	22 AAB36652	Human cytokine rec

#### ALIGNMENTS

RESULT 1  
AAR92814  
ID AAR92814 standard; Protein; 423 AA.  
XX  
AC AAR92814;  
XX  
DT 21-MAY-1996 (first entry)  
XX  
DE Human interleukin-11 receptor alpha chain.

XX  
KW Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;  
KW therapy; diagnosis.  
XX  
OS Homo sapiens.

XX	Key	Location/Qualifiers
FT	Peptide	1..23
FT	Protein	/label= Sig_peptide
FT	Domain	24..423
FT	Domain	/label= Mat_protein
FT	Domain	/label= 24..366
FT	Domain	/note= "the extracellular domain includes haemopoietin and Ig-like domains"
FT	Domain	367..392
FT	Domain	/label= Transmembrane_domain
FT	Domain	393..423
FT	Domain	/label= Cytoplasmic_tail

WO9607737-A1.

14-MAR-1996.

05-SEP-1995; 95WO-AU00578.

```

XX 05-SEP-1994; 94AU-0007902.
PR 05-SEP-1994; 94AU-0007901.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Hilton DJ;
XX
XX WPI: 1996-171612/17.
XX N-PSDB; AAT17869.
XX
XX Nucleic acid encoding haemopoietin receptor containing conserved
XX amino acid motif esp. IL-11 receptor alpha chain - used for
XX developing IL-11 (ant)agonists
XX
XX Claim 8; Page 47-49; 87pp; English.
XX
XX The human interleukin-11 (IL-11) receptor alpha chain (AAR92814)
XX was identified by expression of DNA (AAT17869) isolated from human
XX bone marrow cDNA libraries. Expression of the human IL-11
XX receptor alpha chain results in specific binding of human IL-11
XX and permits IL-11 signalling. The receptor alpha chain can be used
XX to develop agonists or antagonists of therapeutic appin. or in
XX the treatment or diagnosis of conditions involving a deficiency of
XX IL-11, excess IL-11 or aberrant effects of normal endogenous IL-11
XX levels.
XX
XX Sequence 423 AA;
XX
XX Query Match 100.0%; Score 2282; DB 17; Length 423;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-150;
XX Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 1 MSSSCSGLSRVLVAVATALVSASSPCPAWGPVQYQPGRSVKLCCPGVTAGDPVSWF 60
Db 1 mssscglsrvlvavatalvsasspcpawgpgvqyqpggrsvklccpgvtagdpsvswf 60
Oy 61 RDGEPKLLQGPDSGLGHELVLAQADSTDEGTYICQTLGALGGTTLQLGYPARPVWSC 120
Db 61 rdgepkllqgpdsaglghelvlaqadstdegtyicqlldgalggtvtlqlypparpvpsc 120
Oy 121 QAADYENFSCWTSPSQISGLPTRYLTSYRKKTVLGADSQRRSPSTGWPCCQDPLGAARC 180
Db 121 qaadyenfscwtspsqisglptryltsyrkktvlgadsqrrspstgwpccqdpplgaarc 180
Oy 181 VVHGAEFWSQYRINVTENPILGCASTRLLDVSLSILRPDPQGLRVESVFCYRGLRAS 240
Db 181 vvhgafwswqyrinvtenvpilggastrlldvslsilrpdppqglrvsvfcyprglras 240
Oy 241 WTPASWPCQPHLLKFRLOYRPAQHPAWSTVEPAGLEEVITDVAGLPHAVRVSARDEL 300
Db 241 wtpaswpcqphllkfrloyrpaqhpawstvepagleevitdavglyphavrvsarfdl 300
Oy 301 DAGWTSTWSBAMGTPSTGTIPKEIPAWCOLHTQPEVEPQVDSPPAPRPSLQPHRLD 360
Db 301 dagwtstwsbawgtpstgtipkeipawqlhtqpevepqvdsppaprpsslqphrllhdh 360
Oy 361 RDSVEQAVLASLGLSLFLGVLGALALGLLRLRRGKSGKSPKPGFLASVIPPVDRRPGA 420
Db 361 rdsveqavlaslglslflgvlgalalglrlrrrgksgkspkpgflasvipvdrprga 420
Oy 421 PNL 423
Db 421 pnl 423
XX
XX RESULT 2
XX ID AAR99090
XX ID AAR99090 standard; Protein: 422 AA.
XX
XX AC AAR99090;
XX

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DT 09-OCT-1996 (first entry)
XX Human interleukin-11 receptor.
DE
XX
XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;
XX osteoporosis; Paget disease; myeloma.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..23
XX Protein /label= Sig_peptide
XX /label= 24..422
XX Domain /label= Mat_protein
XX /label= 24..365
XX Region /label= Extracellular_domain
XX /label= 24..111
XX Region /label= Ig-like_region
XX /label= 112..365
XX Region /label= Type-1-cytokine_region
XX /label= 366..390
XX Domain /label= Transmembrane_domain
XX /label= 391..422
XX Domain /label= Intracellular_domain
XX
XX W09619574-A1.
XX
XX 27-JUN-1996.
XX
XX 27-NOV-1995; 95WO-US15400.
XX
XX 22-DEC-1994; 94US-0362304.
XX
XX (GEMY ) GENETICS INST INC.
XX
XX Tobin JF;
XX
XX WPI: 1996-309588/31.
XX N-PSDB; AAT33278.
XX
XX New nucleic acid encoding human interleukin 11 receptor - and
XX related protein, antibodies, receptor antagonists, etc, useful for
XX treating and preventing loss of bone mass
XX
XX Claim 13; Page 35-37; 54pp; English.
XX
XX Human interleukin-11 (IL-11) receptor (AAR99090) is thought to play a
XX role in the regulation of bone maturation and repair. Its amino
XX acid sequence was deduced from a cDNA clone (AAT33278) isolated from
XX a human activated peripheral blood mononuclear cell cDNA library.
XX Recombinant IL-11 receptor or its fragments, pref. amino acids
XX 24-422, 24-365 (soluble extracellular domain), 391-422, 102-422 or
XX 102-365, can be expressed in host cell systems. It is used to
XX treat/prevent loss of bone mass (e.g. osteoporosis, Paget's disease,
XX multiple myeloma or hypogonadal conditions), as well as immune
XX diseases and cancer.
XX
XX Sequence 422 AA;
XX
XX Query Match 98.9%; Score 2257.5; DB 17; Length 422;
XX Best Local Similarity 99.5%; Pred. No. 1.4e-148;
XX Matches 421; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Oy 1 MSSSCSGLSRVLVAVATALVSASSPCPAWGPVQYQPGRSVKLCCPGVTAGDPVSWF 60
Db 1 mssscglsrvlvavatalvsasspcpawgpgvqyqpggrsvklccpgvtagdpsvswf 60
Oy 61 RDGEPKLLQGPDSGLGHELVLAQADSTDEGTYICQTLGALGGTTLQLGYPARPVWSC 120
Db 61 rdgepkllqgpdsaglghelvlaqadstdegtyicqlldgalggtvtlqlypparpvpsc 120
Oy 121 QAADYENFSCWTSPSQISGLPTRYLTSYRKKTVLGADSQRRSPSTGWPCCQDPLGAARC 180

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Db 121 qaadyenfctwspqsglplryltsyrkktvlgadsqrrspstgppwpcpdpigaarc 180
Qy 181 VVHGAEFWQYRINVTENPLGASTRLLDVSLQSLRDPDQGLRVESVPGYPRGLRAS 240
Db 181 vvhgafwsgyrynvtvnpl-gastrlldvslqslrpppggrrvesvpyprlras 239
Qy 241 WTPASWPCQPHFLKFRQYRPAQHPAMSTVEPAGLEEVITDAVAGLPHAVRVVSARDFL 300
Db 240 wtpaswpcqphfllkfrlqyrpqahpawstvepagleevitdavaglpahavrvsardfl 299
Qy 301 DAGTWTWSPEAWGTPSTGTIPKEIPAMGOLHTQPEVEPQVDSAPPRESLOPHRLLDH 360
Db 300 dagtwtwspeawgtptstgtipkeipawgqlhtqvevpqvdspapprrpslqphprlldh 359
Qy 361 RDSVEQVAVLASIGLSIFLGLVAGALALGLWLRRLRGKDGSPKPGFLASVIPVDRRPGA 420
Db 360 rdsveqvavlasiglsiflglvagalalglwlrirrgkdgspkpgflasvipvdrpga 419
421 PNL 423
420 pnl 422

RESULT 3
AAB36654
ID AAB36654 standard; Protein; 422 AA.
XX
AC AAB36654;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human IL-11 receptor subunit alpha protein SEQ ID NO:11.
XX
KW DNAX cytokine receptor subunit; DCRS2; receptor protein;
KW modulating cell proliferation; diagnosis; detection; drug screening;
XX immunological disorder.
OS Homo sapiens.
XX
PN WO200073451-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAY-2000; 2000WO-US14867.
XX
PR 01-JUN-1999; 99US-0322913.
(SCHE ) SCHERING CORP.
Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;
WPI; 2001-061536/07.
Novel composition comprising DNAX cytokine receptor subunit polypeptide
useful for regulating immune system function and for treating
immunological disorders
Disclosure; Page 13-15; 93pp; English.
The present invention describes a composition (I) comprising a
recombinant DNAX cytokine receptor subunit-2 (DCRS2), polypeptide.
The DCRS2 polypeptide is useful for binding ligands and for preparing
antibodies. The DCRS2 polypeptide is also useful for modulating cell
proliferation, for diagnostic and therapeutic applications, for
detecting presence of their ligands and in drug screening assays. It
is also useful for treating conditions such as immunological disorders.
The present sequence represents a cytokine receptor subunit protein
which is given in an alignment of various cytokine receptor subunits in
the exemplification of the present invention.
Sequence 422 AA;
XX
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Query Match 98.9%; Score 2257.5; DB 22; Length 422;
Best Local Similarity 99.5%; Pred. No. 1.4e-148;
Matches 421; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 MSSSCGSLSRVLAVATALVSASSPCQAWGPPGVQYQOPGRSVKLCPCGVTAGDPVSWF 60
Db 1 mssscgslsrvlavatalvsasspcqawgppgvqygqgrsvklccpgvtagdpvswf 60
Qy 61 RDEGPKLLQGGDSGLGHVLAQADSTDEGTICQTLDCALGCTVTQLQGYPPARPVVSC 120
Db 61 rdgpkllqgpdsglghelvlaqadstdegticqtldegalgctvtqlqgypparpvsc 120
Qy 121 QAADYENFCTWSPQISGLPTRYLTSYRKKTVLGADSORRSPSTGWPQDPDPLGAARC 180
Db 121 qaadyenfctwspqisglptryltsyrkktvlgadsqrrspstgwpqdpdplgaarc 180
Qy 181 VVHGAEFWQYRINVTENPLGASTRLLDVSLQSLRDPDQGLRVESVPGYPRGLRAS 240
Db 181 vvhgafwsgyrynvtvnpl-gastrlldvslqslrpppggrrvesvpyprlras 239
Qy 241 WTPASWPCQPHFLKFRQYRPAQHPAMSTVEPAGLEEVITDAVAGLPHAVRVVSARDFL 300
Db 240 wtpaswpcqphfllkfrlqyrpqahpawstvepagleevitdavaglpahavrvsardfl 299
Qy 301 DAGTWTWSPEAWGTPSTGTIPKEIPAMGOLHTQPEVEPQVDSAPPRESLOPHRLLDH 360
Db 300 dagtwtwspeawgtptstgtipkeipawgqlhtqvevpqvdspapprrpslqphprlldh 359
Qy 361 RDSVEQVAVLASIGLSIFLGLVAGALALGLWLRRLRGKDGSPKPGFLASVIPVDRRPGA 420
Db 360 rdsveqvavlasiglsiflglvagalalglwlrirrgkdgspkpgflasvipvdrpga 419
Qy 421 PNL 423
Db 420 pnl 422

RESULT 4
AAR92813
ID AAR92813 standard; Protein; 432 AA.
XX
AC AAR92813;
XX
DT 21-MAY-1996 (first entry)
XX
DE Murine interleukin-11 receptor alpha chain.
XX
KW Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
KW therapy; diagnosis.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..23 /label= Sig_peptide
FT Protein 24..432 /label= Mat_protein
FT Domain 24..367 /label= Extracellular_domain
FT /label= "the extracellular domain includes haemopoietin and Ig-like domains"
FT Domain 368..393 /label= Transmembrane_domain
FT Domain 394..432 /label= Cytoplasmic_tail
WO9607737-A1.
14-MAR-1996.
05-SEP-1995; 95WO-AU00578.
XX
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PR 05-SEP-1994; 94AU-0007902.
PR 05-SEP-1994; 94AU-0007901.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Hilton DJ;
XX WPI; 1996-171612/17.
XX N-PSDB; AAT17868.
XX Nucleic acid encoding haemoipoietin receptor containing conserved
PT amino acid motif esp. IL-11 receptor alpha chain - used for
PT developing IL-11 (ant)agonists
XX Claim 6; Page 42-44; 87pp; English.
XX The murine interleukin-11 (IL-11) receptor alpha chain Nrl
CC (AAR92813) was identified by expression of DNA (AAT17868) isolated
CC from adult mouse liver cDNA libraries. Nrl is a low affinity
CC receptor for IL-11 and interacts with gp130 to generate a high
XX affinity IL-11 receptor. IL-11 can be used to develop
XX agonists or antagonists of therapeutic appln. or in the treatment
CC or diagnosis of conditions involving a deficiency of IL-11,
CC excess IL-11 or aberrant effects of normal endogenous IL-11
XX levels.
XX Sequence 432 AA;

Query Match 82.4%; Score 1879.5; DB 17; Length 432;
Best Local Similarity 83.1%; Pred. No. 2e-122;
Matches 353; Conservative 18; Mismatches 51; Indels 3; Gaps 2;

Qy 1 MSSSCGSLRVLVAVATALVSASSPCPAWGPVQYQGRSVKLCPCGVTAGDPVSWF 60
Db 1 mssscgsltrvlavatalvssspcpqawpgvqyqgprpvmllccpgvsagtpvswf 60
Qy 61 RDGEPKLLQGPDGSLGHELVLAQAADSTDEGTYICQTLDGALGGTVTLQGYPPARPVSC 120
Db 61 rdgdrlllqgpdsglghrlvlaqvdsdpgtyvcqtlvgsggmvtlklgfparrpesc 120
Qy 121 QAADYENFSCWSPQISGLPTRYLTSTYRKTKVLGADSORSPSTGPWPCPDPLGAARC 180
Db 121 qavdyenfscwspqvsqglptryltsyrkktlpgaesqrespgwpcpdpleasrc 180
Qy 181 VVHGAEFWSQYRINVTENPNLPGASTRLLDVLSQILRPDPQGLRVESVPGYPRILHAS 240
Db 181 vvhgaeftwseyrinvtenvpl-gastclldvrlsqilrpdppqglrvsvpgyprrlhas 240
Qy 241 WTPASWPCQPHFLKFRQYRPAQHAPWSTVEPAGLEEVITDAVAGLPHAVRVSARDFL 300
Db 240 wtpaswrrqphflklfrlyrpaqhpawstvepgleevitdavaglphavrvsardfl 299
Qy 301 DAGTWSWSPPEAWGTPSTGTIPKEIPAWQLHTQ--PEVEPQVDSPPAPRPSLOPHRLL 358
Db 300 dagtwsawspeawgtpstgtipqdeipdwsqghgqgleavvagedspaparslqdprrl 359
Qy 359 DHRDSVEQVAVLASIGLISFLGVAGALALGLWLRLRGGKDGSPKPGFLASVIPVDRRP 418
Db 360 dhrdpqlegvavlasigfisciglavgalalglwlrirrrsgkdgqpkpallapmpivek1p 419
Qy 419 GAPNL 423
Db 420 g1pnl 424

RESULT 5
AAB36653
ID AAB36653 standard; Protein; 432 AA.
XX
AC AAB36653;
XX
DT 13-MAR-2001 (first entry)

```

```

XX Mouse IL-11 receptor subunit alpha protein SEQ ID NO:10.
DE
XX
XX DNAX cytokine receptor subunit; DCRS2; receptor protein;
KW modulating cell proliferation; diagnosis; detection; drug screening;
KW immunological disorder.
XX
XX Mus sp.
XX
XX WO200073451-A1.
XX
XX 07-DEC-2000.
XX
XX 30-MAY-2000; 2000WO-US14867.
XX
XX 01-JUN-1999; 99US-0322913.
XX (SCHE ) SCHERING CORP.
XX
XX Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan EJ;
XX
XX WPI; 2001-061536/07.
XX
XX Novel composition comprising DNAX cytokine receptor subunit polypeptide
XX useful for regulating immune system function and for treating
XX immunological disorders
XX
XX Disclosure; Page 13-15; 93pp; English.
XX
XX The present invention describes a composition (I) comprising a
XX recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide.
XX The DCRS2 polypeptide is useful for binding ligands and for preparing
XX antibodies. The DCRS2 polypeptide is also useful for modulating cell
XX proliferation, for diagnostic and therapeutic applications, for
XX detecting presence of their ligands and in drug screening assays. It
XX is also useful for treating conditions such as immunological disorders.
XX The present sequence represents a cytokine receptor subunit protein
XX which is given in an alignment of various cytokine receptor subunits in
XX the exemplification of the present invention.
XX
XX Sequence 432 AA;

Query Match 81.2%; Score 1853.5; DB 22; Length 432;
Best Local Similarity 82.1%; Pred. No. 1.2e-120;
Matches 349; Conservative 19; Mismatches 54; Indels 3; Gaps 2;

Qy 1 MSSSCGSLRVLVAVATALVSASSPCPAWGPVQYQGRSVKLCPCGVTAGDPVSWF 60
Db 1 mssscgsltrvlavatalvssspcpqawpgvqyqgprpvmllccpgvsagtpvswf 60
Qy 61 RDGEPKLLQGPDGSLGHELVLAQAADSTDEGTYICQTLDGALGGTVTLQGYPPARPVSC 120
Db 61 rdgdrlllqgpdsglghrlvlaqvdsdpgtyvcqtlvgsggmvtlklgfparrpesc 120
Qy 121 QAADYENFSCWSPQISGLPTRYLTSTYRKTKVLGADSORSPSTGPWPCPDPLGAARC 180
Db 121 qavdyenfscwspqvsqglptryltsyrkktlpgaesqrespgwpcpdpleasrc 180
Qy 181 VVHGAEFWSQYRINVTENPNLPGASTRLLDVLSQILRPDPQGLRVESVPGYPRILHAS 240
Db 181 vvhgaeftwseyrinvtenvsl-gastclldvrlsqilrpdppqglrvsvpgyprrlhas 239
Qy 241 WTPASWPCQPHFLKFRQYRPAQHAPWSTVEPAGLEEVITDAVAGLPHAVRVSARDFL 300
Db 240 wtpaswrrqphflklfrlyrpaqhpawstvepgleevitdavaglphavrvsardfl 299
Qy 301 DAGTWSWSPPEAWGTPSTGTIPKEIPAWQLHTQ--PEVEPQVDSPPAPRPSLOPHRLL 358
Db 300 dagtwsawspeawgtpstgtipqdeipdwsqghgqgleavvagedslaparslqdprrl 359
Qy 359 DHRDSVEQVAVLASIGLISFLGVAGALALGLWLRLRGGKDGSPKPGFLASVIPVDRRP 418
Db 359 dhrdsveqvavlasigfisciglavgalalglwlrirrrsgkdgspkpgflasvipvdrpp 418

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Db 360 dhrcdpleqvavlaslgifscglagvalglwlrirrskegqpkpgllapmipveklp 419  
QY 419 GAPNL 423  
Db 420 gipnl 424  
RESULT 6  
AAR99091  
ID AAR99091 standard; Protein; 441 AA.  
XX AAR99091;  
XX  
XX 09-OCT-1996 (first entry)  
DE Murine Etl-2 gene product.  
XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;  
KW osteoporosis; Paget disease; myeloma; Etl-2.  
Mus sp.  
PN WO9619574-A1.  
XX  
XX  
PD 27-JUN-1996.  
XX  
XX 27-NOV-1995; 95WO-US15400.  
XX  
XX 22-DEC-1994; 94US-0362304.  
XX (GEMY ) GENETICS INST INC.  
XX  
XX Tobin JF;  
XX  
XX WPI: 1996-309588/31.  
DR N-PSDB; AAT32613.  
XX  
XX New nucleic acid encoding human interleukin 11 receptor - and  
PT related protein, antibodies, receptor antagonists, etc, useful for  
PT treating and preventing loss of bone mass  
XX  
XX Example 1; Page 37-40; 54pp; English.  
XX  
XX The amino acid sequence of the murine Etl-2 gene product is given  
CC in AAR99091. Probes based on the Etl-2 gene (AAT32613) were used  
CC to screen a human cDNA library, yielding a cDNA clone (AAT33278) that  
CC coded for human interleukin-11 receptor (AAR99090), a protein  
involved in bone maturation and repair.  
Sequence 441 AA;  
Query Match 79.5%; Score 1813.5; DB 17; Length 441;  
Best Local Similarity 82.7%; Pred. No. 7.4e-118; Indels 3; Gaps 2;  
Matches 339; Conservative 17; Mismatches 51;  
QY 16 ATALVSASSPCQAWGPPGVYQGPGRSVKLCPCGVTAGDPVSWFRDGEKLLQGDGSL 75  
Db 25 atalvsasspcqawgppgvqyggprpvmccpgvsgatpvsfdrdgsrlilgpdsgl 84  
QY 76 GHELVLQAQDSTDEGNYICQTLGALGGTTLQLGYPARPVSVSCQAADYENFSCWSPS 135  
Db 85 ghlvlqaqdsdtegyvycqtlgvgggmvtlklgfparpvscqadvfensctwspg 144  
QY 136 QISGLPTRYLTYSRKKTVLGADSORSPSGPWPQDPLGAARCVVHGAEFWSOYRINV 195  
Db 145 qvsglptryltysrkktcpgaesqrespsctgppwpcqdplesrcvvhgaefwseyrinv 204  
QY 196 TEVNPGLGASTRLIDVLSQILRPDPQGLRVESVPGYPRGLRASWTYPASWPCQPHFL 255  
Db 205 tevnpl-gastcldlvrlgslrpdppqglrvsvpgyprllhaswtypaswrrqphfl 263  
QY 256 KFRLOYRPAQHPAMSTVERAGLEEVITDAVAGLPHAVRVVSARDFLDAGTWTWSPAWGT 315

Db 264 kfrlqyrpadhpawstvepiglietvldavaglpahvrvsarfldagtwsawspawgt 323  
QY 316 PSTGTIPKEIPAMQQLHTQ--PEVEPQVDSPPAPRPSLOPHRLLDHRDSVEQVAVLASL 373  
Db 324 pstgplqdeipdwsgqhgqleavvaqedsaparpqlqdpdrldhrdpleqvavlasl 383  
QY 374 GILSFTGLVAGALALGLWLRRLRGKDGSPKPGFLASVIPVDRRPGAPNL 423  
Db 384 gifscglagvalglwlrirrskgdpgkpgllapmipveklpgipnl 433  
RESULT 7  
AAY59390  
ID AAY59390 standard; Protein; 379 AA.  
XX  
XX AAY59390;  
XX  
XX 14-MAR-2000 (first entry)  
XX  
XX Murine soluble interleukin-11 receptor.  
XX  
XX Interleukin-11; IL-11; IL-11R; human; bone density disorder; gp130;  
KW IL-11 tertiary complex; glycoprotein 130; postmenopausal bone loss;  
KW bone resorption inhibitor; bone formation; therapy.  
XX  
XX Mus sp.  
XX  
XX WO9959608-A2.  
XX  
XX 25-NOV-1999.  
XX  
XX 19-MAY-1999; 99WO-CA00516.  
XX  
XX 19-MAY-1998; 98CA-2237915.  
XX (HAMI-) HAMILTON CIVIC HOSPITAL RES DEV CORP.  
XX  
XX Shaughnessy S, Austin RC;  
XX  
XX WPI: 2000-062377/05.  
DR N-PSDB; AA240400.  
XX  
XX Inhibiting formation of a tertiary complex for the treatment of  
PT osteoporosis  
XX  
XX Example 3; Page 46-50; 61pp; English.  
XX  
XX This sequence is the soluble mouse interleukin-11 receptor (IL-11R).  
CC The invention relates to a method of treating or alleviating the symptoms  
CC of a pathological condition in which bone density is decreased comprises  
CC inhibiting the formation of a tertiary complex of IL-11, IL-11 receptor  
CC and glycoprotein 130 (gp130) in a mammalian patient suffering from such a  
CC condition. The method is used to treat or alleviate the symptoms of a  
CC pathological condition in which bone density is decreased, especially  
CC postmenopausal bone loss. The IL-11 binding peptide is useful in the  
CC purification of IL-11 or in depleting IL-11 from a solution. TRAP  
CC (tartrate-resistant acid phosphatase) and bone marrow formation assays  
CC can be used for the identification of IL-11 antagonists. The method not  
CC only inhibits bone resorption and hence bone loss, but also increases the  
CC process of bone formation to increase bone density.  
XX  
XX Sequence 379 AA;  
Query Match 72.9%; Score 1662.5; DB 21; Length 379;  
Best Local Similarity 83.7%; Pred. No. 1.7e-107;  
Matches 309; Conservative 17; Mismatches 40; Indels 3; Gaps 2;  
QY 1 MSSSCSGLSRVLVAVATALVSASSPCQAWGPPGVYQGPGRSVKLCPCGVTAGDPVSWF 60  
Db 1 mssscsgltrvlvavatalvsssspcqawgppgvqyggprpvmccpgvsgatpvsf 60



PS Disclosure; Page 13-15; 93pp; English.

XX The present invention describes a composition (I) comprising a  
CC recombinant DNA cytokine receptor subunit-2 (DCRS2) polypeptide.  
CC The DCRS2 polypeptide is useful for binding ligands and for preparing  
CC antibodies. The DCRS2 polypeptide is also useful for modulating cell  
CC proliferation, for diagnostic and therapeutic applications, for  
CC detecting presence of their ligands and in drug screening assays. It  
CC is also useful for treating conditions such as immunological disorders.  
CC The present sequence represents a cytokine receptor subunit protein  
CC which is given in an alignment of various cytokine receptor subunits in  
CC the exemplification of the present invention.

XX Sequence 460 AA;

Query Match 17.6%; Score 402; DB 22; Length 460;

Best Local Similarity 30.6%; Pred. No. 3.5e-20;

Matches 144; Conservative 55; Mismatches 184; Indels 88; Gaps 23;

1 MSSSCSLSRVLVAVATATVSSPCQAWGPPGVQYOGPGRSVKLCCPGVTAGDPVS-- 58

2 ltvgctllvallaapaavalvlg--cralevangtvtspgatvtllcpqkeagntih 59

59 WFRDGEPLKLGPD-SGLGHELVLAQADSTDECTYICQTLGALGCTVTLQCYPPARPV 117

60 wysgsgs---qnewttgtntvlrdvqlretgdyic-slnhltvgtvplldvdppeepk 114

118 VSC-QAADYENFSCWTSPSQISGLPTRYLTSYRKKTVLGADSORRSPSTGPMPCP-QDPL 175

115 lscfrknlplnaicewrpsstps-pttkavlfakki-----ntngksdfqpcqysqql 168

176 GAARCVVHGAEFWSQYRI-NVTEVNLPGASTRLDLVSLQSLRPPDPOGLRVESVPGYP 234

169 ksfscqveilegdkvyhivslcvansvsgskshneafhsikmvqpdpnanlvvsaijprp 228

235 RGLRASWTYPASWPCQPHLLKRLQYRPAQHPAWS-----TVEPAGLEEVIITDAVGL 288

229 rwlkvsqhpwtwd-psyillqfryr---pwskeftvlllpvaqvcvindhairgv 283

289 PHAVRVSARDFLDAGTWSTWSPAMGTPTSTGTIPKEIPA---WGQLHTQPEVEPQVDSPA 345

284 khvqvrgkeeldlgqswsepevtgtpwiae-prttpagilwnp--tqvsve---ds-- 335

346 PPRPSLOPHRLDLHRD-----SVEQVAVILA-----SLGILSFLGLVAGALGLW---- 391

336 -----anhdqyessteatsvlapvqessmslptfl-vaggslafglllcvf 382

392 --LRLRRGGKD-----GSPKPGFLASVLPVDRRPGAPN 422

383 ilrlrkqkwkseakesktsppppysigplkptflvllphtphssgsdn 433

RESULT 10

AAR13318

ID AAR13318 standard; Protein; 460 AA.

XX

XX AAR13318;

XX 22-OCT-1991 (first entry)

XX IL-6 receptor.

XX Interleukin.

XX Mus musculus.

XX JP03155795-A.

XX

XX

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XX

XX

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XX

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XX

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XX WO9618416-A1.
PN 20-JUN-1996.
PD
XX
XX PF 15-DEC-1995; 95WO-JP02587.
XX
XX PR 18-AUG-1995; 95JP-0210739.
XX PR 16-DEC-1994; 94JP-0313167.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
PA
XX
XX Koishibara Y, Kuromaru K;
PI
XX WPI; 1996-300392/30.
XX DR N-PSDB; AAT31441.
XX
XX Anti-sense oligo:nucleotide inhibitor against human IL-6R expression
PT - for treatment of e.g. tumours, cancers, rheumatoid arthritis,
PT psoriasis, endo:toxic shock, etc.
XX
XX Claim 2; Page 17-21; 32pp; Japanese.
XX
XX Antisense oligonucleotides may be used to inhibit the expression of
CC the interleukin-6 receptor. Inhibition of expression of the
CC IL-6 receptor is useful in the treatment of kidney tumours, myeloma,
CC Kaposi's sarcoma, rheumatoid arthritis, psoriasis and endotoxic
CC shock. The antisense oligonucleotides are administered at a dosage
CC of 0.1-100mg/kg, pref. 0.1-50 mg/kg.
XX
XX Sequence 468 AA;
XX
XX Query Match 16.2%; Score 370.5; DB 17; Length:468;
XX Best Local Similarity 28.6%; Pred. No. 5.4e-18;
XX Matches 130; Conservative 55; Mismatches 198; Indels 71; Gaps 18;
XX
XX 1 MSSCSGLSRVLAVATATLVASASSPCQAWGPPGVQYGGPGRSVKLCPCGVTAGD--PVS 58
XX 2 IAVGCALLAALAAPGAAL--APRCPAQEVARGVLTSLPGDSVLTCPGVEPEDNATVH 59
XX
XX 59 WFRDGEKPLQCPD-----SGLGHELVLAQADSTDEGTICQTLDCALGGTTLQLG 110
XX 60 W-----LLRKPAAGSHPSRWAGMGRLLIRSVQLHDSGNYSYRA-GRPAGTVHLLVD 111
XX
XX 111 YPARPVVSC-QAADYENFSCWSPQISGLPTRLTYSRKTKVLGADSORSPSTG-PW 168
XX 112 VPPEEPQLSCFRKPSLNVVCEWGRSTPSLT-----KAVLLVRKFGNSPAEDFGE 163
XX
XX 169 PC----PQDPLGAARCVVHGAEFWSQYRINTVEVNPGLGASTRLLDVSLQSLRDPDPOG 224
XX 164 PCQYSQESQKFSQCILAVPEGDS--SFYVSMCVASSVSKSKTKTQFGCGILQDPDPPAN 221
XX
XX 225 LRVESVPGYPRGLRASWTYPASWPCQHPFLKFRLOYRPAQHAWSTVEPAGLEE--VIT 282
XX 222 IIVTAVARNRVLSTWQDPHSWN--SSYRLRFLRYAERSKTKTTVMVKDLQHCVIH 280
XX
XX 283 DAVAGLPHAVRVSARDFLDAGTWTWSPENAGTPTSTGIPKPIPAWGQLHTQPEVEPOVD 342
XX 281 DAWSGLRHVQVIRAQEEFGQGWSEWSPENAGTPTWTES-----RSPPAENEVS 328
XX
XX 343 SPAPRPSLQHPRLLDHRDSVEQVAV----LASIGILSFLGLVAGALALG----- 389
XX 329 TPMQALTNTKDDNII-IRDSANATSLPVQDSSVPLPTFL-VAGGSLAFGTLLCIAIVL 386
XX
XX 390 ----LW-LRLRGGKDGSPKPGFLASVTPVDRRP 418
XX
XX 387 RFKTKWIKIRALKEGKTSMHPPYSLGLVPERPR 420
XX
XX RESULT 12
XX AAP90284
XX ID AAP90284 standard; Protein; 468 AA.
```

```
XX AAP90284;
XX
XX 31-MAR-1992 (first entry)
XX
XX Sequence of a receptor protein for human B cell stimulating
XX factor-2 (BSF2 receptor).
XX
XX B cell; immune disorder; therapy; diagnosis; prophylaxis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH Region 2..22
XX FT /label= hydrophobic region
XX FT Region 362..386
XX FT /label= hydrophobic region
XX
XX EP325474-A.
XX
XX 26-JUL-1989.
XX
XX 20-JAN-1989; 89EP-0300536.
XX
XX 14-JAN-1989; 89JP-0017461.
XX 22-JAN-1988; 88JP-0012387.
XX 25-JAN-1988; 88JP-0012599.
XX 04-AUG-1988; 88JP-0194885.
XX 20-JAN-1989; 89JP-0009774.
XX
XX (KISH/) KISHIMOTO T.
XX
XX Kishimoto T;
XX
XX WPI; 1989-214667/30.
XX DR N-PSDB; AAN90340.
XX
XX Receptor protein for human B cell stimulating factor-2 - obtd. by
XX recombinant DNA techniques and used as diagnostic, prophylactic or
XX therapeutic agent
XX
XX Claim 2; Page 19-21; 63pp; English.
XX
XX The cDNA in AAN90340 was derived from monocyte cell line U937.
XX Isolated BSF2 receptor and DNA encoding it are claimed, as are
XX (b) expression vectors; (c) host organisms; (d) antibodies; and
XX (e) hybridomas.
XX
XX Sequence 468 AA;
XX
XX Query Match 16.1%; Score 367.5; DB 10; Length 468;
XX Best Local Similarity 28.4%; Pred. No. 8.7e-18;
XX Matches 129; Conservative 56; Mismatches 198; Indels 71; Gaps 18;
XX
XX 1 MSSCSGLSRVLAVATATLVASASSPCQAWGPPGVQYGGPGRSVKLCPCGVTAGD--PVS 58
XX 2 IAVGCALLAALAAPGAAL--APRCPAQEVARGVLTSLPGDSVLTCPGVEPEDNATVH 59
XX
XX 59 WFRDGEKPLQCPD-----SGLGHELVLAQADSTDEGTICQTLDCALGGTTLQLG 110
XX 60 W-----VLRKPAAGSHPSRWAGMGRLLIRSVQLHDSGNYSYRA-GRPAGTVHLLVD 111
XX
XX 111 YPARPVVSC-QAADYENFSCWSPQISGLPTRLTYSRKTKVLGADSORSPSTG-PW 168
XX 112 VPPEEPQLSCFRKPSLNVVCEWGRSTPSLT-----KAVLLVRKFGNSPAEDFGE 163
XX
XX 169 PC----PQDPLGAARCVVHGAEFWSQYRINTVEVNPGLGASTRLLDVSLQSLRDPDPOG 224
XX 164 PCQYSQESQKFSQCILAVPEGDS--SFYVSMCVASSVSKSKTKTQFGCGILQDPDPPAN 221
XX
XX 225 LRVESVPGYPRGLRASWTYPASWPCQHPFLKFRLOYRPAQHAWSTVEPAGLEE--VIT 282
XX 222 IIVTAVARNRVLSTWQDPHSWN--SSYRLRFLRYAERSKTKTTVMVKDLQHCVIH 280
XX
XX 283 DAVAGLPHAVRVSARDFLDAGTWTWSPENAGTPTSTGIPKPIPAWGQLHTQPEVEPOVD 342
XX 281 DAWSGLRHVQVIRAQEEFGQGWSEWSPENAGTPTWTES-----RSPPAENEVS 328
XX
XX 343 SPAPRPSLQHPRLLDHRDSVEQVAV----LASIGILSFLGLVAGALALG----- 389
XX 329 TPMQALTNTKDDNII-IRDSANATSLPVQDSSVPLPTFL-VAGGSLAFGTLLCIAIVL 386
XX
XX 390 ----LW-LRLRGGKDGSPKPGFLASVTPVDRRP 418
XX
XX 387 RFKTKWIKIRALKEGKTSMHPPYSLGLVPERPR 420
XX
XX RESULT 12
XX AAP90284
XX ID AAP90284 standard; Protein; 468 AA.
```



Db 222 itvtavarnprwlsvtwqphsw-n-ssfyrlrfelyraersktfttmvkdqlqhcvh 280  
 QY 283 DAVAGLPHAVRSARDFLDAGTWTSTWSPAWGTPSTGTPKEIPAWGQLHTQPEVEPQVD 342  
 Db 281 dawsglrhvqlraeqefggewsewseamgtptwtes-----rspaenevs 328  
 QY 343 SPAPPRSLQPHRLDHRDSVEQVAV-----LASLGILSLGLVAGALALG----- 389  
 Db 329 tpmqalttnkddnll-frdsanatslpvqdsstsvlptfl-vagsglafgtllciaivl 386  
 QY 390 ----LW-LRLRRGGKDGSPKPGFLASVIVPDRRP 418  
 Db 387 rfkktwklralkegktsmhpypyslgqlvperprp 420  
 RESULT 13  
 AAR37215  
 ID AAR37215 standard; Protein; 468 AA.  
 XX  
 AC AAR37215;  
 XX  
 DE IL-6 receptor.  
 XX  
 DE Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncated;  
 KW transmembrane; multiple myeloma; binding; ability; signal transfer;  
 KW disease; intracellular.  
 XX  
 OS Synthetic.  
 XX  
 PN JP05091892-A.  
 XX  
 PD 16-APR-1993.  
 XX  
 PF 02-OCT-1991; 91JP-0255521.  
 XX  
 PR 02-OCT-1991; 91JP-0255521.  
 XX  
 PA (CHUS) CHUGAI PHARM CO LTD.  
 PA (KISH/) KISHIMOTO C.  
 PA (TOYJ) TOSOH CORP.  
 XX  
 DR WPI; 1993-161739/20.  
 DR N-PSDB; AAQ41746.  
 XX  
 PT New interleukin-6 receptor deriv. - for treating diseases caused  
 by IL-6, e.g. multiple myeloma  
 XX  
 Disclosure; Page 10-12; 23pp; Japanese.  
 XX  
 CC This sequence represents an interleukin-6 (IL-6) receptor. Variants  
 CC of the receptor lacking either the immunoglobulin-like domain or the  
 CC transmembrane and intracellular domain have IL-6 binding ability and  
 CC signal transfer ability. Either the full length or truncated IL-6  
 CC receptors may be used for diseases caused by IL-6 such as multiple  
 CC myeloma.  
 XX  
 SQ Sequence 468 AA;  
 Query Match 16.1%; Score 367.5; DB 14; Length 468;  
 Best Local Similarity 28.4%; Pred. No. 8.7e-18;  
 Matches 129; Conservative 56; Mismatches 198; Indels 71; Gaps 18;  
 QY 1 MSSSGLSRLVAVATALVSASPCQAWGPPGVGYGPGRSVKLCCPGVTAGD--PVS 58  
 Db 2 lavgcallaapgaal--aprrcpagvargvitslpdgsvtlcpvpednatvh 59  
 QY 59 WFRDGEPLKLOGPD-----SGLGHELVLAQADSTDECTYICQLDGLGALGTVTILQIG 110  
 Db 60 w-----virkpaagshpsrwagmrrllrsvqlhdsgnyscyra-grpdtgthllvd 111

QY 111 YPPARPVSC-QAADYENFSCWSPSQISGLPTRYLTSTYRKKTIVLGADSORRSPSTG-PW 168  
 Db 112 vpbeeqblscfrksplsnvvcwgrstpsltt-----kavllvrkfqnspsaedfge 163  
 QY 169 PC----PQDPLGAARCVVHGAEPWISOYRINVTENVPLGGASTRLLDVSLQSIILRPDPQ 224  
 Db 164 pcysgeskfcslavpegds--sfyismcvassvsgskfstqtqfqcglqdpdp 221  
 QY 225 LRVESYPGYPRGLRASWTYPASWPCQPHFLKFLQYRPAQHPAWSTVEPAGLEE--VIT 282  
 Db 222 itvtavarnprwlsvtwqphsw-n-ssfyrlrfelyraersktfttmvkdqlqhcvh 280  
 QY 283 DAVAGLPHAVRSARDFLDAGTWTSTWSPAWGTPSTGTPKEIPAWGQLHTQPEVEPQVD 342  
 Db 281 dawsglrhvqlraeqefggewsewseamgtptwtes-----rspaenevs 328  
 QY 343 SPAPPRSLQPHRLDHRDSVEQVAV-----LASLGILSLGLVAGALALG----- 389  
 Db 329 tpmqalttnkddnll-frdsanatslpvqdsstsvlptfl-vagsglafgtllciaivl 386  
 QY 390 ----LW-LRLRRGGKDGSPKPGFLASVIVPDRRP 418  
 Db 387 rfkktwklralkegktsmhpypyslgqlvperprp 420  
 RESULT 14  
 AAB36655  
 ID AAB36655 standard; Protein; 468 AA.  
 XX  
 AC AAB36655;  
 XX  
 DE 13-MAR-2001 (first entry)  
 XX  
 DE Human IL-6 receptor subunit alpha protein SEQ ID NO:12.  
 XX  
 KW DNAX cytokine receptor subunit; DCRS2; receptor protein;  
 KW modulating cell proliferation; diagnosis; detection; drug screening;  
 KW immunological disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200073451-A1.  
 XX  
 PD 07-DEC-2000.  
 XX  
 PF 30-MAY-2000; 2000WO-US14867.  
 XX  
 PR 01-JUN-1999; 99US-0322913.  
 XX  
 PA (SCHE) SCHERING CORP.  
 XX  
 PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;  
 XX  
 DR WPI; 2001-061536/07.  
 XX  
 PT Novel composition comprising DNAX cytokine receptor subunit polypeptide  
 PT useful for regulating immune system function and for treating  
 PT immunological disorders  
 XX  
 PS Disclosure; Page 13-15; 93pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a  
 CC recombinant DNAX cytokine receptor subunit-2;(DCRS2) polypeptide.  
 CC The DCRS2 polypeptide is useful for binding ligands and for preparing  
 CC antibodies. The DCRS2 polypeptide is also useful for modulating cell  
 CC proliferation, for diagnostic and therapeutic applications, for  
 CC detecting presence of their ligands and in drug screening assays. It  
 CC is also useful for treating conditions such as immunological disorders.  
 CC The present sequence represents a cytokine receptor subunit protein  
 CC which is given in an alignment of various cytokine receptor subunits in  
 CC the exemplification of the present invention.  
 XX  
 SQ Sequence 468 AA;

Query Match 16.1%; Score 367.5; DB 22; Length 468;  
Best Local Similarity 28.4%; Pred. No. 8.7e-18;  
Matches 129; Conservative 56; Mismatches 198; Indels 71; Gaps 18;

QY 1 MSSSGSLSRVLAVAVATLVASASSPCQAWGPPGVQYQGRSVKLCPCGVTAGD--PVS 58  
DB 2 lavgcallaallaagaal--aprrcpagvargvltalpgdsvltcpgvepednatvh 59  
QY 59 WFRDGEPLKLOGPD-----SGLGHELVLAQADSTDEGTICQTLGAGLGGTVTLQLG 110  
DB 60 W-----VLRKpaagshpsrwagmgrrlllrsqvlhdsngyscyra-grpagtvlhllvd 111  
QY 111 YPARPVVSC--QAADYENFSCWTSQISGLTPRLTSLYRKKTVLGDADSRSPSTG-PW 168  
DB 112 vppeepqiscfrksplsnvvcwgrprstpsltt-----kavllvrkfgspaedfge 163  
QY 169 PC-----PODPLGAARCVVHGAEFWQYRINVTENVNPLGGASTRLLDVSLQSLRDPDPQG 224  
DB 164 pcqysgesqkfcqlavpegds--sfyivmcvassvsgskfktqtfgcgilqdpdpan 221  
QY 225 LVESVPGYPRGLRASWTYPASWPCOPHLLKFRLOYRPAQHAWSTVEPAGLEE--VIT 282  
DB 222 itvtavarnprwlsvtwqphswn--ssfyrlrfelryraersktfttmvkdqlghcvih 280  
QY 283 DAVAGLPHAVRYSAARDFLDAGTWSTWSPWAGTTPGTIPKEIPAWGOLHTQPEVEPQVD 342  
DB 281 dawsglrhvvglrageefggqgsewseamgtptwtes-----rspgaenevs 328  
QY 343 SPAPPRLPSLQHPRLDHRDSVEQVAV-----LASLGILSFLGLVAGALALG----- 389  
DB 329 tpmqaltknkddnil-frdsenatslpvqdsessvplptfl-vagsglafgtllciaiavl 386  
QY 390 ----LW-LRLRGGKDGSPKPCFLASVIPVDRRP 418  
DB 387 rfkktkiralkegktsmhppyslgqlvperprp 420

RESULT 15

AAR20024  
ID AAR20024 standard; Protein; 372 AA.

AC AAR20024;

DT 31-MAR-1992 (first entry)

XX Ciliary neurotrophic factor receptor.

KW CNTFR; transgenic animal; motoneurone disease; trauma;  
XX muscular dystrophy; inflammation; amyotrophic lateral sclerosis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 42..90

FT /note= "Ig-like"

FT Domain 116..294

FT /note= "cytokine receptor-like"

XX WO9119009-A.

XX 12-DEC-1991.

XX 03-JUN-1991; 91WO-US03896.

XX 15-MAY-1991; 91US-0700677.

PR 01-JUN-1990; 90US-0532285.

XX 28-MAR-1991; 91US-0676647.

XX (REGE-) REGENERON PHARM INC.

XX Davis S, Squinto S, Furth M, Yancopoulos GD;

XX WPI; 1992-007490/01.  
DR N-PSDB; AAQ20195.  
XX DNA encoding CNTF receptors - useful in diagnosis, physiological  
PT study and treatment of CNTF-related disorders  
XX Claim 16; Fig 2; 92pp; English.  
XX The CNTFR has an Ig-like domain fused to the N-terminus of the  
CC proposed factor binding domain via a short acidic tether. The  
CC protein is structurally similar to IL-6 receptor.  
XX Sequence 372 AA;

Query Match 16.1%; Score 366.5; DB 13; Length 372;  
Best Local Similarity 30.0%; Pred. No. 7.8e-18;  
Matches 122; Conservative 47; Mismatches 168; Indels 69; Gaps 16;

QY 12 LVAVATLVASASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPSVFRDGEPLKLOGP 71  
DB 12 vlaaaaavvyqrhspqe--aphvgyerlgsdvtlpcgtanwdaavtrvngtd---lap 66  
QY 72 DSGLGHELVLAQADSTDEGTICQTLDG--ALGGTVTLQLGYPPARPVWSCQAADY-ENFS 129  
DB 67 dlilngsqvlhglelghsglyacfhrrdswlhrhqvllhvglpprepviscrantypkgfy 126  
QY 130 CTWSPSQISGLPT-RYLTSYRKKTVLGDADSRSPSTGFWPCQDPLGAARCVVHGAEFW 188  
DB 127 cswh-----lptptyipntfnvtvlhgsk-----lmvcekdpalknchrhymhlf 172  
QY 189 S--QYRINVTENVNPLGGASTRLLDVSLQSLRDPDPQGLRVESVPGYPRGLRASWTYPAS 246  
DB 173 stikykvsvsnaighnataitfdef-tlvkdpdenvvarpvpsnprlvtwtqtpst 231  
QY 247 WPCQPHLLKFRLOYRPAQHAWSTVEPA-GLEEYITDAVAGLPHAVRYSAARDFLDAGTW 305  
DB 232 wdpesfplkfllyrplldqwhveisdgtahitdayagkeyliqvaakd-neigtw 290  
QY 306 STWSPWANGTPTGTIPKEIPAWGOLHTQPEVEPOVDSAPPRLPSLQHPRLLDHRDSVE 365  
DB 291 sdwsvaahatpwtee-prhlhtteaq--aaettststslapp-----pttkicd----- 336  
QY 366 QVAVLASLGILSFLGLVAGALALGLWLRGGKDGSPKPGFLASV 411  
DB 337 -----ppql-----gsgggpcapflvsv 354

Search completed: August 24, 2001, 17:32:31

Job time: 114 sec

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Qy 104 TVTLQLGYPPARP-VWSCQAADYENFECTWSPQISGLPTRYLTSYRKKTVLGADSQRRS 162

Search completed: August 24, 2001, 17:34:12  
Job time: 155.sec

```
Db 149 RNMKDUTCRWTPGAHGETLHTNYSLSKYLRWYQDNTCEEYHTVGPCHSHPKD----- 203
QY 179 RCVVHGAERWSQYRINVTENPLGGASTRLDVSLOSILRPPDQGLRVESVPGYPRGLR 238
Db 204 -----LALFTPEIWEATNRNLCGARSVDLTLDVLDVTTDPPDVHVSRRVGGLEDQLS 257
QY 239 ASWTYPASWPCQPHFL--KFLQYRPAQHPAWSTYEP-----AGLEEVITDAVAG 287
Db 258 VRWVSP---PALKDFLQAKYQIRYRVEDSVDMKVVDVDSYNTQTSCLAGLK-----PG 307
QY 288 LPHAVRVSARDP-----LDAGTWSTWS-PEA-----WGTPSTGTIP 322
Db 308 TVYFVQVRNCFGIYKKGAGIWSHSTAASTPRSPRPGPGGGVCEPRGGPSSGPRV 367
QY 323 KEIP---AWGOLH 332
Db 368 RELKQFLGLKX 380

RESULT 12
ID 046561 PRELIMINARY; PRT: 581 AA
AC 046561; P79205; 046574; 046573; P79203; 046569;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (PRLR) (OPR).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=HAMMARY GLAND, AND LIVER;
RX MEDLINE=98001468; PubMed=9343303;
RA Bignon C., Binart N., Ormandy C., Schuler L.A., Kelly P.A., Djiane J.;
RT "Long and short forms of the ovine prolactin receptor: cDNA cloning
and genomic analysis reveal that the two forms arise by different
alternative splicing mechanisms in ruminants and in rodents.";
RT J. Mol. Endocrinol. 19:109-120(1997).
RN [2]
RP SEQUENCE OF 61-395 FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=SCOTTISH BLACKFACE / ISOLATE M22/80; TISSUE=ANTERIOR PITUITARY;
RX MEDLINE=99049302; PubMed=9832462;
RA Tortorese D.J., Brooks J., Ingletton P.M., McNeilly A.S.;
RT "Detection of prolactin receptor gene expression in the sheep
pituitary gland and visualization of the specific translation of the
signal in gonadotrophs.";
RL Endocrinology 139:5215-5223(1998).
RN [3]
RP SEQUENCE OF 147-302 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=FETAL LIVER, AND CORPUS LUTEUM;
RA Anthony R.V., Smith G.W., Duong A., Pratt S.L., Smith M.F.;
RT "Two forms of the prolactin receptor messenger ribonucleic acid are
present in ovine fetal liver and adult ovary.";
RL Endocrine 3:291-295(1995).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
PRLACTIN (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: THREE ISOFORMS; LONG ISOFORM (L-OPR) (SHOWN
HERE). SHORT ISOFORM (S-OPR) AND SOLUBLE ISOFORM; ARE PRODUCED BY
ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED (LIVER,
PITUITARY, ADRENAL GLAND, OVARY AND FETAL LIVER).
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
DR EMBL: AF041257; AAB96795.1; -
DR EMBL: AF041977; AAB96920.1; -
DR EMBL: AF041979; AAB97082.1; -
DR EMBL: AF042358; AAB97744.1; -
DR EMBL: AF042358; AAB97743.1; -
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DR EMBL: AF041978; AAB96965.1; -
DR EMBL: Y10578; CAA71597.1; -
DR EMBL: Y10808; CAA71766.1; -
DR HSSP: P14787; IAN3.
DR InterPro: IPR001777; -
DR InterPro: IPR002996; -
DR InterPro: IPR003528; -
DR Pfam: PF00041; fn3; 2.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW ALTERNATIVE SPLICING.
FT SIGNAL 1 24
FT CHAIN 25 581
FT DOMAIN 25 237
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 258
FT DOMAIN 259 581
FT DOMAIN 259 581
FT DOMAIN 123 227
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 132 132
FT VARSPLIC 24 66
FT VARSPLIC 67 581
FT VARSPLIC 286 296
FT VARSPLIC 297 581
FT CONFLICT 281 281
FT CONFLICT 387 387
FT SEQUENCE 581 AA; 65235 MW; EC534FDE538837A0 CRC64;
SQ
Query Match 9.3%; Score 212; DB 6; Length 581;
Best Local Similarity 26.8%; Pred. No. 2.5e-08;
Matches 61; Conservative 35; Mismatches 96; Indels 36; Gaps 9;
QY 112 PPARP-VVSCQADYENFSCVSPQISGLPTRYLTYSRKKTVLGGADSORRSTGPNWC 170
DB 27 PPEKPKLIKRSFGKETFTCWMEPGADGLPTNYTYRKE-----GETLIHCC 75
QY 171 PQDPLGAACVHVHGADEF---WSQYRINVTENPLGGASTRLDVSLOSILRPPDQGLRV 227
DB 76 PDYKGGPNSCVFSKXYTSIWKMYVITVSAINQMGISSDPLVDVYTYVEPEPPNLT 135
QY 228 ESWPGYPRG--LRASWTYP-----ASWPCQPHFLKFLQYRPAQHPAWST--VEPAGE 278
DB 136 ELKHPEDRKPYLWIKWSPTLTDVKSGW-----FSIQYEIRLKPKEKATDWTHTFAPKLQ 190
QY 279 EVITDAVAGLPHAVRVSARDPDLADAGTWSTWSPEAWGTPSTGTIPKEIP 326
DB 191 LKIFNLPQGYLVQIRCKP--DHGYWSEWSPE-----SFIQIPNDP 231
RESULT 13
ID O18880 PRELIMINARY; PRT: 296 AA.
AC O18880;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR SHORT FORM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97375450; PubMed=92311767;
RA Schuler L.A., Nagel R.J., Gao J., Horseman N.D., Kessler M.A.;
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DR HSP; p40189; 1BOU.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
KW Signal; Receptor.
FT CHAIN 37
FT SIGNAL 38
SQ SEQUENCE 422 AA; 46301 MW; AD9DFCB01B84228 CRC64;

Query Match
Best Local Similarity 9.6%; Score 219; DB 4; Length 422;
Matches 91; Conservative 52; Mismatches 147; Indels 94; Gaps 18;

QY 7 GLSRVLVAVATVAVASASSPCQAWPGVQVQGPCRSVKLCC-----PGVTAGDPVSWF 60
DB 30 GAPRAGSAGHTAVISPQDPTLLI-----GSSLATCSVHGDDPPGATA--EGLYWT 77
QY 61 RDGE---PKLQGPDSGLGHELVLAQAD-----STDEGTIICOTLDGALGGTVTTLQLGY 112
DB 78 LNGRRLPELSRVLNAS---TLALALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 134
QY 113 PARPV-VSCQAADYENFSCWSPSQ--ISGLPTRYLTYSRKTKTVLGADSORRSPSTGWP 169
DB 135 PEKPNINISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEEYHTVGP 194
QY 170 C--PODPLGARCVRVHGAFFWSOYRINVTENPLGGASTRLLDVLSQSLTLRPDPPQGLRV 227
DB 195 CHIPKD-----LALFTPYEIWEATNRLGARSDDLTLDDLDVVTTPDPPDVHV 243
QY 228 ESVGPGYRGLRASWTYPASWPCQPHLL--KRLQYRPAQHPAWSTVEP-----AG 276
DB 244 SRVGLEQLSVRWVSP---PALKDFLQAKYQIRYVEDSVDMKVVDVDSVNOTSCRLAG 300
QY 277 LEEVITDAVAGLPHAVRVSARDF-----LDAGTWSTWS-PEA-----312
DB 301 LK-----PGTVYEVQVRCNPFGIYSGKAGINSEWSHPTAASPRSERPGPGGGACEP 353
QY 313 -WGTPSTGTIPKEIP---AWGOLH 332
DB 354 RGEFSSGPRRELKQFLGWLKKH 377

RESULT 10
Q9UHH5
ID Q9UHH5 PRELIMINARY; PRT; 422 AA.
AC Q9UHH5:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CLASS I CYTOKINE RECEPTOR.
GN ZCYTOR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lok S., Presnell S.R., Jernberg A.C., Gilbert T., Whitmore T.E.,
RA Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;
RE Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178684; AAD54385.1; -.
DR HSP; p40189; 1BOU.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 422 AA; 46315 MW; 0D2C5F7A01B942EE CRC64;

Query Match
Best Local Similarity 9.6%; Score 218; DB 4; Length 422;
Matches 91; Conservative 52; Mismatches 147; Indels 94; Gaps 18;

QY 7 GLSRVLVAVATVAVASASSPCQAWPGVQVQGPCRSVKLCC-----PGVTAGDPVSWF 60
DB 30 GAPRAGSAGHTAVISPQDPTLLI-----GSSLATCSVHGDDPPGATA--EGLYWT 77
QY 61 RDGE---PKLQGPDSGLGHELVLAQAD-----STDEGTIICOTLDGALGGTVTTLQLGY 112
DB 78 LNGRRLPELSRVLNAS---TLALALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 134
QY 113 PARPV-VSCQAADYENFSCWSPSQ--ISGLPTRYLTYSRKTKTVLGADSORRSPSTGWP 169
DB 135 PEKPNINISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEEYHTVGP 194
QY 170 C--PODPLGARCVRVHGAFFWSOYRINVTENPLGGASTRLLDVLSQSLTLRPDPPQGLRV 227
DB 195 CHIPKD-----LALFTPYEIWEATNRLGARSDDLTLDDLDVVTTPDPPDVHV 243
QY 228 ESVGPGYRGLRASWTYPASWPCQPHLL--KRLQYRPAQHPAWSTVEP-----AG 276
DB 244 SRVGLEQLSVRWVSP---PALKDFLQAKYQIRYVEDSVDMKVVDVDSVNOTSCRLAG 300
QY 277 LEEVITDAVAGLPHAVRVSARDF-----LDAGTWSTWS-PEA-----312
DB 301 LK-----PGTVYEVQVRCNPFGIYSGKAGINSEWSHPTAASPRSERPGPGGGACEP 353
QY 313 -WGTPSTGTIPKEIP---AWGOLH 332
DB 354 RGEFSSGPRRELKQFLGWLKKH 377

RESULT 10
Q9UHH5
ID Q9UHH5 PRELIMINARY; PRT; 422 AA.
AC Q9UHH5:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CLASS I CYTOKINE RECEPTOR.
GN ZCYTOR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lok S., Presnell S.R., Jernberg A.C., Gilbert T., Whitmore T.E.,
RA Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;
RE Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178684; AAD54385.1; -.
DR HSP; p40189; 1BOU.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 422 AA; 46315 MW; 0D2C5F7A01B942EE CRC64;

Query Match
Best Local Similarity 9.5%; Score 217; DB 11; Length 425;
Matches 89; Conservative 52; Mismatches 140; Indels 92; Gaps 17;

QY 17 TALVSASSPCQAWPGVQVQGPCRSVKLCC-----PGVTAGDPVSWFRDGEKLLQ 70
DB 43 TAVISPQDPTLLI-----GSSLQATCSIHGDDPPGATA--EGLYWT 88
QY 71 PDSGLGHELVLAQADSTDEGT-----YICQTLGALGGTVTTLQGYPPARPV-VSCOA 122
DB 89 ELSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEKPFNISCWS 148
QY 123 ADYENFSCWSPSQ--ISGLPTRYLTYSRKTKTVLGADSORRSPSTGWPFC--PODPLGAA 178

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RESULT 7
Q14213 PRELIMINARY; PRT; 229 AA.
AC Q14213;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CYTOKINE RECEPTOR PRECURSOR.
GN EBI3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96135230; PubMed=8551575;
RA Devergne O., Hummel M., Koepfen H., Le Beau M.M., Nathanson E.C.,
RA Kieff E., Birkenbach M.;
RT "A novel interleukin-12 p40-related protein induced by latent Epstein-
RT Barr virus infection in B lymphocytes.";
RL J. Virol. 70:1143-1153(1996).
DR EMBL: L08187; AAA93193.1; -.
DR InterPro: IPR001777; -.
DR InterPro: IPR002996; -.
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
KW Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 229 CYTOKINE RECEPTOR.
SQ SEQUENCE 229 AA; 25391 MW; F42875A4815D81C7 CRC64;

Query Match 10.7%; Score 244; DB 4; Length 229;
Best Local Similarity 30.8%; Pred. No. 3.2e-11;
Matches 73; Conservative 35; Mismatches 95; Indels 34; Gaps 11;

QY 94 CPTLDGALGGTTLQLGYPPAR---PWSCOAADYE-NFSCWTS---PSQISGLPTRYLTS 147
DB 15 CPPCSRKG-----PPAALTLPVQCRASRYPIAVDCSWLPPAPNSPSPVFSFIAT 65
QY 148 YRKKTVLGADSQRRSPSTGPWCPDPLGAARCVVHGAEFWSQ--YRINVTENPLGGAS 205
DB 66 YR---LGMAARGH-----WPCLOQTPSTSTCTITDVLFSMAPVVLNVTAHPWGSSS 116
QY 206 TRLLDVSLOSILRPDPQGLRVESVPGYPRGLRASWTYPASWPCQPHFLKFLQRYRPAQ 265
DB 117 S-FVPTTEHIKDPPEGVRLS--PLAERHVQVQVQWEPFGSNWPFPEIFSLKYWIRYKROG 173
QY 266 HPAMSTVEPAGLEEVITDAVAGLPHA---VRVSARDFLDAGTWSTWSPAWGTPSTG 319
DB 174 AARFHRVGPIEATSFILRAVR--PRARYVQVAQDLTDYGLSDWSLPATATMSLG 228

RESULT 8
O57519 PRELIMINARY; PRT; 881 AA.
AC O57519;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE GPI30P1.
GN XGP130.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen J., Grace A., Chien K.R.;
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RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF041845; AAC03531.1; -.
DR HSSP: P40189; 1BOU.
DR InterPro: IPR001777; -.
DR InterPro: IPR002996; -.
DR InterPro: IPR003529; -.
DR Pfam: PF00041; fn3; 4.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
SQ SEQUENCE 881 AA; 99003 MW; 7DE7942D211138A0 CRC64;

Query Match 9.8%; Score 223; DB 13; Length 881;
Best Local Similarity 23.3%; Pred. No. 5.7e-09;
Matches 88; Conservative 61; Mismatches 146; Indels 82; Gaps 18;

QY 1 MSSSCSGLSRVLVAVATALVSASSPCPAWPGVQYQGPCRSVKLCCPGVTA----GDP 56
DB 5 ISFFCLISSVVLIVHOAELVKV---CGRIFFDPGIVHGERPETA-YCVINQTCREDASR 60
QY 57 VSMFRDG-----EPKLLOGPDSGLGHELVLQAQADSTDEGTVICQTL-DGALGGT---VT 106
DB 61 IYWLKGVKVPETQYELNQTTSVTFENL-----TTLASPLTCNVMSHVAANTLYGIF 115
QY 107 LQLGYPPARPV-VSCQAADYENFSCWTSQISGLPRVLTYSYRKKTVLGADSQRRSPST 165
DB 116 FTGLPPDKPTNLTCIVYNODNLCTWDCGRPTNLTNTVLTSLR-WAHFGANCYRGANNS 174
QY 166 GWPCCPDPLGAARCVVH--GAEFWSQYRINVTENPLGAGSTRLLDVSLOSILRDPQPQ 223
DB 175 -----CTIHSPPGFYIDTTFQVEATRELGIQKSETLTIDPVNIVKPNPQ 220
QY 224 GLRVESVPGYPRGLRASWTYPASWPCQPHFLKFLQRYRPAOHPAWSTV-----EP 274
DB 221 LSELISLLELPNALKIEWKNPIT---NAFNLYNRYRPVKTDQWEMPEEDTASHRDS 276
QY 275 AGLEEVITDAVAGLPHAVRSARDFLDAGTWSTWS-----PEAWGTPSTGTIPKEIPA 327
DB 277 FTLDLPLNTVVEV--SIRCIHKD--GHGFWSDWSLKKQVTPTEA--PPSRG----- 322
QY 328 WQQLHTQPEVEQVDSF 344
DB 323 -----PDIWKKIDSP 332

RESULT 9
O75462 PRELIMINARY; PRT; 422 AA.
AC O75462;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CYTOKINE-LIKE FACTOR-1 PRECURSOR.
GN CLF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Elson G.C.A., Graber P., Losberger P., Herren S., Gretener D.,
RA Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.F.;
RT "CLF-1, a Novel Soluble Protein Shares Homology With Members of the
RT Cytokine Type-I Receptor Family.";
RN J. Immunol. 0:0-0(1998).
RP SEQUENCE FROM N.A.
RA Magrangeas F., Jacques Y., Minvielle S.;
RT "Cloning and expression of a novel soluble protein containing
RT hematopoietic cytokine receptor domains.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF059293; AAC28335.1; -.
DR EMBL: AF073515; AAD39681.1; -;
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DR InterPro: IPR003530; -.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00047; 1g; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW SIGNAL.
FT CHAIN 1 20 POTENTIAL.
FT CHAIN 21 336 CILIARY NEUROTROPHIC FACTOR RECEPTOR
FT CHAIN 21 336 ALPHA.
SQ SEQUENCE 372 AA; 40831 MW; EB75A9EE6A1BB8C8 CRC64;

Query Match 16.4%; Score 373.5; DB 11; Length 372;
Best Local Similarity 31.5%; Pred. No. 7e-21;
Matches 112; Conservative 49; Mismatches 164; Indels 31; Gaps 13;

QY 1 MSSSCGLSRVLAVATALVSASSPCPAWGPVQVQGPGRSVKLCPCGTAGDPVSWF 60
DB 1 MTASVPWACCAVLAANAAYVTKISQOB--APHVOYERLGADVTLPCCGTASWDAAVTWR 58
QY 61 RDGEPLKLGQDGLGHELVLAQADSTDEGTICQTLDG-ALGGTVTLQLGYPPARPVVS 119
DB 59 VNGTD--LAPDLNGSQLILRLSLGSLGYACFRDSWHLRHQVLLHVGLPPREPVL 115
QY 120 QQAADY-ENFSTWSPSQISGLPT-RYTSYKTKVVLGADSORRSPSTGWPCCPODPLGA 177
DB 116 CRSNTYPRGFYSWH-----LPTPTIYPNTFNVTVLHGSK-----IMVCKDPAK 161
QY 178 ARCVVHGAEFWS--QYRINVTENVPLGGASTRLLDVLSQILRPDPQGLRVESVPGYPR 235
DB 162 NCCHRYWHLFSTIRKYSVISVSNAL-GHNTAITTDEFTIVKPPDENNVARVPSPNPR 220
QY 236 GLRASVTYPASWPCOPHFLKFRLOYPRAQHPAWSTVEPA-GLEEVITDAVAGLPHAVRV 294
DB 221 RLEVWQPTSTWPDSPESPLKEFLRYPLLDQHWELSDGTAHTITDAYAGKEYITQV 280
QY 295 SARDELDAGTWSPEAWGTSTGTIPKEIPAWQLHTQPEVQVDSPPAPRPS 350
DB 281 AAKD-NEIGTWSWVAHAATPWTEE-PRHLTTEAQ---APETTTSTTSSLAPPPT 331

RESULT 5
ID O35228 PRELIMINARY; PRT; 228 AA.
AC O35228;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE CYTOKINE RECEPTOR-LIKE MOLECULE.
GN EBT3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Nomura H., Yaguchi N., Hanyuu C., Maeda M., Kikuchi Y., Nakata Y.,
RA Kojima T., Tulin E.E., Hasegawa M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF013114; AAB67115.1; -.
DR MGD; MGI:1354171; EBI3.
DR InterPro; IPR000282; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003530; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 228 AA; 25353 MW; 49DEFA4E5C4F2126 CRC64;

Query Match 11.5%; Score 261.5; DB 11; Length 228;
Best Local Similarity 35.3%; Pred. No. 1.4e-12;
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Matches 72; Conservative 33; Mismatches 76; Indels 23; Gaps 9;

QY 114 ARPVSCQAADYE-NFSCTWSPSQI--SGLPTRYLTSYRKKTVLGADSORRSPSTGWPWC 170
DB 28 SOPRVQCHASRYPPAVDCSWTLPQAPNSTSTSFATYR---LGVATQOQSQO-----PC 78
QY 171 PODPLGAARCVVHGAEFWS--QYRINVTENVPLGGASTRLLDVLSQILRPDPQGLRVY 228
DB 79 LQSPQASRCTIPDVHLFSTVPYMLNVTAVHP-GGASSLLAFVAERIIPKPPPEGVRLR 137
QY 229 SVPGYPRGLRASWTYPASWPCOPHFLKFRLOYPRAQHPAWSTVEPAGLEEVIITDAVAGL 288
DB 138 TA---GQRLQVLWHPASPMPFPDIFSLKRLYRRRGASHFRQVGP--IEATFTLRNSK 192
QY 289 PHA---VRVSARDEFLDAGTWSTWS 309
DB 193 PHAKYCIQVSAQDLTDYCKPDSWS 216

RESULT 6
ID O75269 PRELIMINARY; PRT; 229 AA.
AC O75269;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE HUMAN CYTOKINE RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lanerding J.E., McCreedy P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Gaines J.,
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RL "Sequence analysis of a 2.5 Mb region in 19p13.3.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005578; AAC33488.1; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003530; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 229 AA; 25396 MW; CFBAD72D91859EF0 CRC64;

Query Match 10.8%; Score 247; DB 4; Length 229;
Best Local Similarity 31.2%; Pred. No. 1.9e-11;
Matches 74; Conservative 34; Mismatches 95; Indels 34; Gaps 11;

QY 94 CQTLGALGGTVTLQLGYPPAR---PVVSCQAADYE-NFSCTWSS--PSOISGLPTRYLTS 147
DB 15 CPPCSGRKG-----PPAALTLPVOCRASRTPIAVDCSWTLPQAPNSTSTSFATY 65
QY 148 YRKKTVLGADSORRSPSTGWPCCPDPLGAARCVVHGAEFWSQ---YRINVTENVPLGGAS 205
DB 66 YR---LGMAARGHS-----WPCLOQTPTSTCTITDVOLFSPMAPVVLNVTAVHPWGS 116
QY 206 TRLLDVLSQILRPDPQGLRVESVPGYPRGLRASWTYPASWPCOPHFLKFRLOYPRAQ 265
DB 117 S-FVPFITEHIIPKPPPEGVRLS--PLAERQLQVQWEPGSPFPFIFESLKIWIYRK 173
QY 266 HPASTVTEPAGLEEVIITDAVAGLPHA---VRVSARDEFLDAGTWSTWSPEAWCTPSTG 319
DB 174 AARFHRVGPTEATSFILRAVR--PRARYVYVQAQDLTDYGELSDWSLPAATATNSLG 228
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DR Pfam; PF00047; ig; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
DR SMART; SM0060; FN3; 1.
SQ SEQUENCE 422 AA; 45222 MW; 1F8BC05C139FC326 CRC64;

Query Match      98.9%; Score 2257.5; DB 4; Length 422;
Best Local Similarity 99.5%; Pred. No. 1.1e-164;
Matches 421; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MSSSCGSLRVLAVATLVASSPCQAWGPPGVQYQGPGRSVKLCPCGVTAGDPVSWF 60
DB 1 MSSSCGSLRVLAVATLVASSPCQAWGPPGVQYQGPGRSVKLCPCGVTAGDPVSWF 60
QY 61 RDGEKLLQGGPSGLGHELVLAQADSTDEGTYICQTLGALGGTTLQLGYPARPVYSC 120
DB 61 RDGEKLLQGGPSGLGHELVLAQADSTDEGTYICQTLGALGGTTLQLGYPARPVYSC 120
QY 121 QAADYENFSCWSPSQISGLPTRYLTSYRKKTVLGADSORRSPSTGMPQDPLGAARC 180
DB 121 QAADYENFSCWSPSQISGLPTRYLTSYRKKTVLGADSORRSPSTGMPQDPLGAARC 180
QY 181 VVHGAEFWSQYRINVTENPLGASTRLLDVLSQILRPDPQGLRVESVPGYPRGLRAS 240
DB 181 VVHGAEFWSQYRINVTENPLGASTRLLDVLSQILRPDPQGLRVESVPGYPRGLRAS 240
QY 241 WTYPASWPCQHPFLKFRLOYRPAQHPAWSITVEPAGLEEVITDAVAGLPHAVRVARSDFL 300
DB 241 WTYPASWPCQHPFLKFRLOYRPAQHPAWSITVEPAGLEEVITDAVAGLPHAVRVARSDFL 300
QY 301 DAGTWTSTWSPAWGTPSTGTIPKEIPAWQLHTQPEVEPQVDSPPAPRPSLQPHRLLDH 360
DB 301 DAGTWTSTWSPAWGTPSTGTIPKEIPAWQLHTQPEVEPQVDSPPAPRPSLQPHRLLDH 360
QY 361 RDSVEQVAVLASGLSLFGLVAGALGLWLRGKGKDGSPKGFGLASVLPVDRRGA 420
DB 361 RDSVEQVAVLASGLSLFGLVAGALGLWLRGKGKDGSPKGFGLASVLPVDRRGA 420
QY 421 PNL 423
DB 420 PNL 422

RESULT 2
Q64385 PRELIMINARY; PRT; 432 AA.
AC Q64385;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NR1) (ETL2)
DE (IL-11RALPHA) (IL11RAL).
GN IL11RAL OR IL11RA OR ETL2 OR ETL12/IL11 REC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=LIVER;
RX MEDLINE=95045367; PubMed=7957045;
RA Hilton D.J., Hilton A.A., Raicevic A., Rakar S., Harrison-Smith M.,
RA Gough N.M., Begley C.G., Metcalf D., Nicola N.A., Willson T.A.;
RT "Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130
RL for high affinity binding and signal transduction.";
RL EMBO J. 13:4765-4775(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C, AND C57BL/6; TISSUE=EMBRYO;
RA Neuhaus H., Bettenhausen B., Billinski P., Simon-Chazottes D.,
RA Guenet J.L., Gossler A.;
RL Dev. Biol. 166:521-542(1994).
RN [3]

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RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C, AND C57BL/6;
RA Gossler A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97129000; PubMed=8973540;
RA Billinski P., Hall M.A., Neuhaus H., Gissel C., Heath J.K., Gossler A.;
RT "Two differentially expressed interleukin-11 receptor genes in the
RL mouse genome.";
RL Biochem. J. 320:359-363(1996).
CC -!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11. BINDS TO IL-11
CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE IG-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC EMBL; X74953; CAA52908.1; -
DR EMBL; U14412; AAG53248.1; -
DR EMBL; X94162; CAA63873.1; -
DR EMBL; X94163; CAA63873.1; JOINED.
DR MGD; MGI:107426; Il11ral.
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003006; -
DR InterPro; IPR003530; -
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
DR SMART; SM0060; FN3; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 23
FT CHAIN 24 432
FT DOMAIN 24 367
FT TRANSMEM 368 393
FT DOMAIN 394 432
FT DOMAIN 41 102
FT CARBOHYD 127 127
FT CARBOHYD 194 194
SQ SEQUENCE 432 AA; 46655 MW; 068389943502BBFC CRC64;

Query Match      82.4%; Score 1879.5; DB 11; Length 432;
Best Local Similarity 83.1%; Pred. No. 8.1e-135;
Matches 353; Conservative 18; Mismatches 51; Indels 3; Gaps 2;

QY 1 MSSSCGSLRVLAVATLVASSPCQAWGPPGVQYQGPGRSVKLCPCGVTAGDPVSWF 60
DB 1 MSSSCGSLRVLAVATLVASSPCQAWGPPGVQYQGPGRSVKLCPCGVTAGDPVSWF 60
QY 61 RDGEKLLQGGPSGLGHELVLAQADSTDEGTYICQTLGALGGTTLQLGYPARPVYSC 120
DB 61 RDGEKLLQGGPSGLGHELVLAQADSTDEGTYICQTLGALGGTTLQLGYPARPVYSC 120
QY 121 QAADYENFSCWSPSQISGLPTRYLTSYRKKTVLGADSORRSPSTGMPQDPLGAARC 180
DB 121 QAADYENFSCWSPSQISGLPTRYLTSYRKKTVLGADSORRSPSTGMPQDPLGAARC 180
QY 181 VVHGAEFWSQYRINVTENPLGASTRLLDVLSQILRPDPQGLRVESVPGYPRGLRAS 240
DB 181 VVHGAEFWSQYRINVTENPLGASTRLLDVLSQILRPDPQGLRVESVPGYPRGLRAS 240
QY 241 WTYPASWPCQHPFLKFRLOYRPAQHPAWSITVEPAGLEEVITDAVAGLPHAVRVARSDFL 300
DB 241 WTYPASWPCQHPFLKFRLOYRPAQHPAWSITVEPAGLEEVITDAVAGLPHAVRVARSDFL 300
QY 301 DAGTWTSTWSPAWGTPSTGTIPKEIPAWQLHTQPEVEPQVDSPPAPRPSLQPHRLLDH 360
DB 301 DAGTWTSTWSPAWGTPSTGTIPKEIPAWQLHTQPEVEPQVDSPPAPRPSLQPHRLLDH 360
QY 361 RDSVEQVAVLASGLSLFGLVAGALGLWLRGKGKDGSPKGFGLASVLPVDRRGA 420
DB 361 RDSVEQVAVLASGLSLFGLVAGALGLWLRGKGKDGSPKGFGLASVLPVDRRGA 420
QY 421 PNL 423
DB 420 PNL 422

RESULT 2
Q64385 PRELIMINARY; PRT; 432 AA.
AC Q64385;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NR1) (ETL2)
DE (IL-11RALPHA) (IL11RAL).
GN IL11RAL OR IL11RA OR ETL2 OR ETL12/IL11 REC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=LIVER;
RX MEDLINE=95045367; PubMed=7957045;
RA Hilton D.J., Hilton A.A., Raicevic A., Rakar S., Harrison-Smith M.,
RA Gough N.M., Begley C.G., Metcalf D., Nicola N.A., Willson T.A.;
RT "Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130
RL for high affinity binding and signal transduction.";
RL EMBO J. 13:4765-4775(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C, AND C57BL/6; TISSUE=EMBRYO;
RA Neuhaus H., Bettenhausen B., Billinski P., Simon-Chazottes D.,
RA Guenet J.L., Gossler A.;
RL Dev. Biol. 166:521-542(1994).
RN [3]

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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: August 24, 2001, 17:34:11 ; Search time 37.87 Seconds  
(without alignments)  
1477.820 Million cell updates/sec

Title: US-09-532-263-5  
Perfect score: 282  
Sequence: 1 MSSCSGLSRVLVAVATLV.....KPGFLASVIVDRRPGAPNL 423

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL16.\*

- 1: sp-archaea.\*
- 2: sp-bacteria.\*
- 3: sp-fungi.\*
- 4: sp-human.\*
- 5: sp-invertebrate.\*
- 6: sp-mammal.\*
- 7: sp-mhc.\*
- 8: sp-organelle.\*
- 9: sp-phage.\*
- 10: sp-plant.\*
- 11: sp-rodent.\*
- 12: sp-unclassified.\*
- 13: sp-vertebrate.\*
- 14: sp-virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2257.5	98.9	422	4	Q16542
2	1879.5	82.4	432	11	Q64385
3	1853.5	81.2	432	11	P70225
4	373.5	16.4	372	11	O88507
5	261.5	11.5	228	11	O35228
6	247	10.8	229	4	O75269
7	244	10.7	229	4	O14213
8	223	9.8	881	13	O57519
9	219	9.6	422	4	O75462
10	218	9.6	422	4	Q9UHH5
11	217	9.5	425	11	Q9JTM58
12	212	9.3	581	6	O46561
13	207	9.1	296	6	O18880
14	195	8.5	611	13	Q9PTH9
15	191.5	8.4	227	6	Q9GLW3
16	191.5	8.4	346	13	O93404
17	191	8.4	206	4	Q16354
18	190	8.3	611	13	Q9PTI0
19	190	8.3	611	13	Q9IBF6

20	189.5	8.3	349	4	Q9UHH5
21	189	8.3	538	13	Q9DFU0
22	186	8.2	625	6	Q9X592
23	184.5	8.1	622	6	Q9NOJ7
24	182.5	8.0	327	11	Q9ET05
25	179.5	7.9	327	6	Q9TT18
26	179.5	7.9	638	13	Q9DE08
27	170	7.4	918	13	Q9W6U9
28	170	7.4	1280	13	Q9O933
29	160	7.0	198	6	O18985
30	160	7.0	600	13	Q9PTP0
31	159	7.0	217	6	O46386
32	153.5	6.7	1256	11	Q9ET59
33	152.5	6.7	1242	11	Q9QZS7
34	152.5	6.7	1256	11	Q9JIX1
35	151.5	6.6	1234	11	Q9R044
36	151.5	6.6	1252	11	Q9QX7
37	151.5	6.6	1252	11	Q9JIX2
38	150	6.6	329	4	Q9OQ41
39	144.5	6.3	1948	4	Q13332
40	138.5	6.1	335	11	Q9R278
41	138.5	6.1	1241	4	O60500
42	138	6.0	1162	11	Q9QW3
43	138	6.0	1898	11	Q84604
44	138	6.0	1898	11	Q9EQI7
45	137.5	6.0	335	11	Q9QUM1

## ALIGNMENTS

RESULT 1

Q16542	PRELIMINARY;	PRT;	422 AA.
AC	Q16542	Q14626;	
DT	01-NOV-1996 (TREMELREL. 01, Created)		
DT	01-NOV-1996 (TREMELREL. 01, Last sequence update)		
DE	01-MAR-2001 (TREMELREL. 16, Last annotation update)		
DE	INTERLEUKIN-11 RECEPTOR.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=MUSCLE;		
RX	MEDLINE=95399754; PubMed=7670098;		
RA	Cherel M., Sorel M., Lebeau B., Dubois S., Moreau J.F., Bataille R.,		
RA	Minvielle S., Jacques Y.;		
RT	"Molecular cloning of two isoforms of a receptor for the human		
RL	hematopoietic cytokine interleukin-11.";		
RL	Blood 86:2534-2540(1995).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Van Leuven F., Stas L., Hilliker C., Miyake Y., Gossler A.;		
RL	Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE OF 3-390 FROM N.A.		
RC	TISSUE=PLACENTA;		
RA	Cherel M., Sorel M., Dubois S., Lebeau B., Moreau J., Jacques Y.,		
RL	Minvielle S.;		
CC	Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.		
CC	-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX		
CC	DOMAIN.		
DR	EMBL; U32324; AAB36492.1; -		
DR	EMBL; U32324; AAB36492.1; -		
DR	EMBL; U32323; AAB36491.1; -		
DR	EMBL; U32323; AAB36491.1; -		
DR	InterPro; IPR001777; -		
DR	InterPro; IPR002996; -		
DR	InterPro; IPR003006; -		
DR	InterPro; IPR003530; -		
DR	Pfam; PF00041; fn3; 2.		

Q9uh15	homo sapien
Q9dfu0	sparus aura
Q9x592	trichosurus
Q9noj7	callithrix
Q9et05	marmota mon
Q9tt18	ovis aries
Q9de08	oncorhynch
Q9w6u9	gallus gall
Q9o933	gallus gall
O18985	cervus elap
Q9tp0	carassius a
O46386	mustela vis
Q9et59	mus musculu
Q9qz57	mus musculu
Q9jix1	mus musculu
Q9r044	rattus norv
Q9qx7	rattus norv
Q9jix2	rattus norv
Q9uq41	homo sapien
Q13332	homo sapien
Q9r278	rattus norv
O60500	homo sapien
Q9qwg3	mus musculu
Q84604	r protein-t
Q9eqi7	mus musculu
Q9qum1	mus musculu

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CC EMBL; J04510; AAA31457.1; -
DR PIR; A30304; A30304.
DR PDB; 1AN3; 03-DEC-97.
DR InterPro; IPR000950; -
DR InterPro; IPR001777; -
DR Pfam; IPR002465; -
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat; 3D-structure.
FT SIGNAL 1 24 BY SIMILARITY
FT CHAIN 25 616 PROLACTIN RECEPTOR.
FT DOMAIN 25 234 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 235 258 POTENTIAL.
FT DOMAIN 259 616 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 122 FIBRONECTIN TYPE-III.
FT DOMAIN 124 227 FIBRONECTIN TYPE-III.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 616 AA; 68840 MW; 800E3166FE7108C CRC64;
SQ
Query Match 8.6%; Score 195.5; DB 1; Length 616;
Best Local Similarity 27.3%; Pred. No. 2e-06;
Matches 65; Conservative 28; Mismatches 98; Indels 47; Gaps 13;
QY 112 PPARP-VVSCQADYENFSCWSPSQISGLPTRYLSYRKTKVLGADSRSPSTGWPC 170
DB 27 PPGKPIFKRSPEKETFTCWMPRGADGLPTNTYLTTHKE-----GETITHEC 75
QY 171 PDPLGAARCVVHG---AEPWSYRINVTENVPLGG--ASTRLLDVLSLOSILRPDPQGL 225
DB 76 PDYKGTGPNSCYCSKKHSTLSWTIYITVNTATNGMSVSDPRVDVY--IVPDPDPVNL 133
QY 226 RVESVCPYGRG---LRASWTYP-----ASWPCQPHFLKRLQYRPAQHPAWSTVPAGL 277
DB 134 TLEVKHPEDRKPLWYKWLPPTLVDVRSWG-----LTLQYEIRLKEPAKEWET-HFAQG 187
QY 278 EE--VTDAVAGLPHAVRSARDELDAQYWSWSPAWGTPTGTTP-----KEIPAW 328
DB 188 QTOFKILSLYPGOKYLVQRCKP--DHGFWSVMSPE-----SSIQIPNDFMTMKDITVW 238
RESULT 14
PRLR_RAT
ID PRLR_RAT STANDARD; PRT; 610 AA.
AC P05710; Q63451; Q63723; Q62832; Q64274; Q63479;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (LACTOGEN RECEPTOR).
GN PRLR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE-91155946; PubMed-2293032;
RA Shirota M., Banville D., Ali S., Jolicoeur C., Boutin J.M.,
RA Edery M., Djiane J., Kelly P.A.;
RT "Expression of two forms of prolactin receptor in rat ovary and
RT liver.";
RL Mol. Endocrinol. 4:1136-1143(1990).
[2]
RN SEQUENCE FROM N.A. (LONG FORM AND SHORT FORM).
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Ovary;
RX MEDLINE-90241201; PubMed-2159291;
RA Zhang R., Buczek E., Tsai-Morris C.H., Hu Z.Z., Dufau M.L.;
RT "Isolation and characterization of two novel rat ovarian lactogen

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RT receptor cDNA species.";
RL Biochem. Biophys. Res. Commun. 168:415-422(1990).
[3]
RN SEQUENCE OF 281-610 FROM N.A.
RA Banville D., Stocco R., Murthy K.K., Boie Y., Kelly P.A.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (MEDIUM FORM).
RP TISSUE=Liver;
RC MEDLINE-88165059; PubMed-2832068;
RA Boutin J.-M., Jolicoeur C., Okamura H., Gagnon J., Edery M.,
RA Shirota M., Banville D., Dusanter-Fourt I., Djiane J., Kelly P.A.;
RT "Cloning and expression of the rat prolactin receptor, a member of
RT the growth hormone/prolactin receptor gene family.";
RN Cell 53:69-77(1988).
[5]
RN SEQUENCE FROM N.A. (FORM NB2).
RP TISSUE=Lymphoma;
RC MEDLINE-92041834; PubMed-1718958;
RA Ali S., Pelligrini I., Kelly P.A.;
RT "A prolactin-dependent immune cell line (Nb2) expresses a mutant form
RT of prolactin receptor.";
RL J. Biol. Chem. 266:20110-20117(1991).
[6]
RN SEQUENCE FROM N.A. (FORM NB2).
RP MEDLINE-95014432; PubMed-7929319;
RA O'Neal K.D., Yu-Lee L.Y.;
RT "Differential signal transduction of the short, Nb2, and long
RT prolactin receptors. Activation of interferon regulatory factor-1 and
RT cell proliferation.";
RL J. Biol. Chem. 269:26076-26082(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING OF THE PRLR GENE.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; M57668; AAA41938.1; -
DR EMBL; M34083; AAA79273.1; -
DR EMBL; L48060; AAA79274.1; -
DR EMBL; U34730; AAA92053.1; -
DR EMBL; M19304; AAA41937.1; -
DR EMBL; W74152; AAA41946.1; -
DR EMBL; U07567; AAA61784.1; -
DR PIR; A29884; A29884.
DR HSSP; P16471; 1BP3.
DR InterPro; IPR000950; -
DR InterPro; IPR001777; -
DR InterPro; IPR002465; -
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 610 PROLACTIN RECEPTOR.
FT DOMAIN 20 229 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 230 253 BY SIMILARITY.
FT DOMAIN 254 610 CYTOPLASMIC (BY SIMILARITY).
FT DOMAIN 20 117 FIBRONECTIN TYPE-III.
FT DOMAIN 119 222 FIBRONECTIN TYPE-III.
FT DISULFID 31 41 BY SIMILARITY.
FT DISULFID 70 81 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .).

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FT	DOMAIN	123	227	FIBRONECTIN TYPE-III.
FT	DISULFID	36	46	BY SIMILARITY.
FT	DISULFID	75	86	BY SIMILARITY.
FT	CARBOHYD	59	59	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	132	132	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	233	233	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE	581 AA; 65159 MW; 975E47CB63CF28EC CRC64;		

Query Match 8.8%; Score 201; DB 1; Length 581;  
Best Local Similarity 26.3%; Pred. No. 7.9e-07;  
Matches 60; Conservative 31; Mismatches 101; Indels 36; Gaps 9;

QY	112	PPARP-VVSCQAADYENFSCWSPSQISGLTPRLTYLTSYRKKTIVLGADSQRRSPSTGWPWC	170
DB	27	PPGPKTIKCRSPGKETFTCWEPGSDGGLPTNTLYHKE-----GETLIHEC	75
QY	171	PQDPLGARNCVVHG---AEFWQYRINVTENVPLGGASTRLLDVSLQSIIRPDPQGLRV	227
DB	76	PDYKTGPNPFCYFSKHTSIWKIYIVITVNAINGVSSDPLXVDVYTVIYEPEPANLTL	135
QY	228	ESVPGYPRG--LRASWTYP-----ASWPCQPHFLKFLQYRPAQHPANSTVEPAGLEE	279
DB	136	ELKHPEDRKPYLWKVFPPLTVDKSGW-----FMIOYEIRLPKETAADWEIHPAAKQTQ	190
QY	280	V-ITDAVAGLPHAVRYARSDFLDAGTWSTWSPAWGTPSTCTPIKEIP	326
DB	191	LKTFSLYPGKYLQVVRCKP--DHGYWSEWSPE-----SSIOIPNDPFP	231

RESULT 13  
PRLR\_RABIT STANDARD; PRT; 616 AA.

ID	PRLR_RABIT	AC	PL4787;
DC	01-APR-1990 (Rel. 14, Created)		
DT	01-APR-1990 (Rel. 14, Last sequence update)		
DT	15-JUL-1998 (Rel. 36, Last annotation update)		
DE	PROLACTIN RECEPTOR PRECURSOR (PRL-R).		
GN	PRLR		
OS	Oryctolagus cuniculus (Rabbit)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9986;		
ON	SEQUENCE FROM N.A.		
RP	TISSUE=Mammary gland;		
RC	MEDLINE=89184578; PubMed=2928321;		
RX	Edery M., Jolicoeur C., Levi-Meyuets C., Dusanter-Fourt I.,		
RA	Petitou B., Boutin J.M., Lesueur L., Kelly P.A., Djiane J.;		
RT	"Identification and sequence analysis of a second form of prolactin		
RT	receptor by molecular cloning of complementary DNA from rabbit		
RT	mammary gland.;"		
RL	Proc. Natl. Acad. Sci. U.S.A. 86:2112-2116(1989).		
RN	[2]		
RP	3D-STRUCTURE MODELING OF 30-228.		
RX	MEDLINE=97248733; PubMed=9094747;		
RA	Halaby D., Thoreau E., Djiane J., Mornon J.P.;		
RT	"Homology modeling of rabbit prolactin hormone complexed with its		
RT	receptor.;"		
RL	Proteins 27:459-468(1997).		
CC	-!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE		
CC	PROLACTIN.		
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		
CC	-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.		
CC	-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.		
CC	-----		
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CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announcement/">http://www.isb-sib.ch/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		
CC	-----		



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DR InterPro; IPR001777; -.
DR Pfam; PF00041; fn3; 4.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 1 23
FT DOMAIN 24 831
FT TRANSMEM 24 438
FT DOMAIN 439 459
FT DOMAIN 460 831
FT DOMAIN 25 122
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 91
FT CARBOHYD 91 100
FT CARBOHYD 100 112
FT CARBOHYD 112 132
FT CARBOHYD 132 162
FT CARBOHYD 262 303
FT CARBOHYD 303 315
FT CARBOHYD 315 335
FT CARBOHYD 335 355
FT SEQUENCE 831 AA; 94394 MW; 220916320F77FAC1 CRC64;

Query Match 10.4%; Score 236.5; DB 1; Length 831;
Best Local Similarity 29.6%; Pred. No. 4.2e-09;
Matches 80; Conservative 35; Mismatches 118; Indels 37; Gaps 13;

QY 113 PARP-VVSCQAADYENFSCWSPQISGLPTRYLTYSRKKTVLGADSRSPSTGPWPCP 171
DB 28 PGKPKIIRCSLEKETFTSCWKKPGSDGLPTNYTLFYSK-----DSEKI-----YEC 76

QY 172 Q-DPLGAARCVVH--AEFWSQYRINVTENVPLGASTRLDVSLSQILRPPDGLRVE 228
DB 77 DYRTSGPNCSYFNRYNTSWTTNTYATNIGSNSSDPQYVDVTSIVQPSVNLTL 136

QY 229 SVPGYPR--GLRASWTYPASWPCQPHLLKFLRQYRPAQHPAWSTVEPAGLEE--VITDA 284
DB 137 T-QRYANIMYLAKWSPPLADASNHLHYELRLKPEEKSEWTV-PVGVTQCKINRL 194

QY 285 VAGLPHAVRSARDFLDAGTWSPEAWGTSTGTIPKEIPAWGLHTQPEVE----- 338
DB 195 NAGMRVYVQV--RCMLDPCGEWSESSERRILISGGLSPPEKPTITKRS-PEKETFTCW 251

QY 339 -QVDSPPAPRSLQHPRLLDHRSVEQV 367
DB 252 KPGLDGGHTNTY-----LLYSKEGEQV 275

RESULT 9
PRLR_COLLI ID PRLR_COLLI STANDARD; PRT; 830 AA.
AC Q90374;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cropsac;
RX MEDLINE=94283267; PubMed=7516866;
RA Chen X., Horseman N.D.;
RT "Cloning, expression, and mutational analysis of the pigeon prolactin
receptor.";
```

```
RL Endocrinology 135:269-276(1994).
-!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
PROLACTIN.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC -----
CC EMBL: U07694; AAA20646.1; -.
DR HSP: P16471; IBP3.
DR InterPro; IPR000950; -.
DR InterPro; IPR001777; -.
DR Pfam; PF00041; fn3; 4.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 1 23
FT DOMAIN 24 830
FT TRANSMEM 24 439
FT TRANSMEM 440 460
FT DOMAIN 461 830
FT DOMAIN 25 122
FT DOMAIN 123 226
FT DOMAIN 229 326
FT DOMAIN 327 429
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 91
FT CARBOHYD 91 100
FT CARBOHYD 100 112
FT CARBOHYD 112 132
FT CARBOHYD 132 163
FT CARBOHYD 263 304
FT CARBOHYD 304 316
FT CARBOHYD 316 336
FT CARBOHYD 336 356
FT SEQUENCE 830 AA; 94507 MW; 3B074E83CDF69EFF CRC64;

Query Match 9.8%; Score 222.5; DB 1; Length 830;
Best Local Similarity 29.3%; Pred. No. 3.9e-08;
Matches 67; Conservative 31; Mismatches 98; Indels 33; Gaps 10;

QY 111 YPARPVVSCQAADYENFSCWSPQISGLPTRYLTYSRKKTVLGADSRSPSTGPWPCP 170
DB 27 YPGKPKIIRCSLEKETFTSCWKKPGSDGLPTNYTLFYSK-----DSEKI-----YEC 75

QY 171 PODPL-GAARCVV--HGAEFWQYRINVTENVPLGASTRLDVSLSQILRPPDGLRVE 227
DB 76 PDYGMSPGNSCYFDKNHTNPTTYNTVMAMNEIGSNSSDPQYVDVTSIVQDPAPVNL 135

QY 228 ESVGYPGRCLRASWTY-PASWPCQ-----HFLKFLRQYRPAQHPAWSTVEPAGLEE 279
DB 136 ETKTS-----ASTTYLLAKWSPPLADVTSNHYRYELRLKPEEKSEWTVS-VGVQT 188

QY 280 --VITDAVAGLPHAVRSARDFLDAGTWSPEAWGTSTGTIPKEIP 326
DB 189 QYKVARLQGVYVQV--RCVLDIGEWSEWSESRHIHPNGESPPEKP 235

RESULT 10
PRLR_CHICK ID PRLR_CHICK STANDARD; PRT; 831 AA.
AC Q04594;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
```



CC BLOOD MONONUCLEAR CELLS AND WEAKLY FOUND IN URINE AND SERUM.  
 CC -!- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE  
 CC N-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.  
 CC -!- PTM: A SHORT SOLUBLE FORM MAY ALSO BE RELEASED FROM THE MEMBRANE  
 CC BY PROTEOLYSIS.  
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD126 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd126.htm"  
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DR EMBL; X12830; CAA31312.1; -;  
 DR EMBL; X58298; CAA41231.1; -;  
 DR EMBL; S72848; AAC60635.1; -;  
 DR PIR; A41242; A41242;  
 DR PIR; JU0080; JU0080;  
 DR PIR; S14621; S14621;  
 DR PIR; S17468; S17468;  
 DR MIM; I47880; -;  
 DR InterPro; IPR000950; -;  
 DR InterPro; IPR001777; -;  
 DR InterPro; IPR002465; -;  
 DR InterPro; IPR003006; -;  
 DR Pfam; PF00041; fn3; 1;  
 DR Pfam; PF00047; ig; 1;  
 DR PROSITE; PS01354; HEMATOPO\_REC\_L\_F3; 1;  
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;  
 KW Alternative splicing; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 468 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.  
 FT DOMAIN 20 365 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 366 386 POTENTIAL.  
 FT DOMAIN 387 468 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 40 103 IG-LIKE C2-TYPE DOMAIN.  
 FT DISULFID 25 193  
 FT DISULFID 47 96  
 FT DISULFID 121 132  
 FT DISULFID 165 176  
 FT CARBOHYD 55 55  
 FT CARBOHYD 93 93  
 FT CARBOHYD 221 221  
 FT VARSPLIC 356 365  
 FT VARSPLIC 366 468  
 FT VARSPLIC 121 121  
 FT MUTAGEN 122 122  
 FT MUTAGEN 132 132  
 FT MUTAGEN 134 134  
 FT MUTAGEN 140 140  
 FT MUTAGEN 153 153  
 FT MUTAGEN 165 165  
 FT MUTAGEN 174 174  
 FT MUTAGEN 176 176  
 FT MUTAGEN 184 184  
 FT MUTAGEN 190 190  
 FT MUTAGEN 193 193  
 FT MUTAGEN 211 211  
 FT MUTAGEN 217 217

FT MUTAGEN 232 232 R->S: 30% DECREASE OF LIGAND-BINDING AND IL6 SIGNALING.  
 FT MUTAGEN 233 233 W->O: 30% DECREASE OF LIGAND-BINDING AND INCREASE OF IL6 SIGNALING.  
 FT MUTAGEN 254 254 E->A: 50% DECREASE OF LIGAND-BINDING AND IL6 SIGNALING.  
 FT MUTAGEN 277 277 C->D: 30% INCREASE OF LIGAND-BINDING AND 100% INCREASE IN IL6 SIGNALING.  
 FT MUTAGEN 278 278 V->N: 50% DECREASE OF LIGAND-BINDING AND 50% INCREASE IN IL6 SIGNALING.  
 FT MUTAGEN 279 279 I->D: COMPLETE LOSS OF LIGAND-BINDING.  
 FT MUTAGEN 280 280 H->I: NO CHANGE OF LIGAND-BINDING AND NO IL6 SIGNALING.  
 FT MUTAGEN 281 281 D->G: 70% DECREASE OF LIGAND-BINDING AND NO IL6 SIGNALING.  
 FT MUTAGEN 285 285 G->D: 80% DECREASE OF LIGAND-BINDING AND NO IL6 SIGNALING.  
 FT MUTAGEN 291 291 Q->K: COMPLETE LOSS OF LIGAND-BINDING.  
 FT MUTAGEN 293 293 R->G: COMPLETE LOSS OF LIGAND-BINDING.  
 SQ SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1B8B CRC64;  
 Query Match 16.1%; Score 367.5; DB 1; Length 468;  
 Best Local Similarity 28.4%; Pred. No. 2.3e-18;  
 Matches 129; Conservative 56; Mismatches 198; Indels 71; Gaps 18;  
 QY 1 MSSSCGLSRVLVAVATLVASASPQAWGPPGVQYQGRSVKLCPCGTAGD--PVS 58  
 DB 2 LAVGCALLAALLAAPGAAL--APRCPAQAEVARGVLTSLPGDSVTLTCEGVPEADNATVH 59  
 QY 59 WFRDGEPLKLGPD-----SGLHELVLQAQADSTDEGTVCOTLDGALGGTVTLQGL 110  
 DB 60 W-----VLKPAAGSHPSRWAGMRLLRSVLHDSGNYSYRA-GRPAGTVHLLVD 111  
 QY 111 YPARPVVSC-QAADYENFSCVTSQISGLPTRLVLTYSRKTKVLGADSORSPSTG-PW 168  
 DB 112 VPPEEPQLSCFRKSPLSNVVCEWGRSTPSLT-----KAVLLVRKFQNSPADFOE 163  
 QY 169 PC-----PQDPLGAARCVVHGAEFWSQYRLNVTVEVNPGLGASTRLDVLDSLQSLRPDPQ 224  
 DB 164 PCOYSQESQKSCQLAVPEGDS--SFYIVSMCVASVSGSKFSTOTFOGCGILQDPAN 221  
 QY 225 LRVESVPGYPRGLRASWTYPASWPCQPHFLKFRLOYRPAQHPAWSTVEPAGELE--VIT 282  
 DB 222 ITVTAVARNPRLSVTWQDPHWSN--SSFYRLRFLRYRAERSKTFETTMVKDLQHCVIH 280  
 QY 283 DAVAGLPHAVRVSRDFLDAGTWTWSPFAMGCTPTGTIPKEIPAWGOLHTOPEVPEPOVD 342  
 DB 281 DAWSLRHVVQLRAQEEFGGSEMSPEAMGTPMTES-----RSSPAENEVS 328  
 QY 343 SPAPRPSLQPHRLLDHRDSVEQVAV-----LASLGLSFLGLVAGALAG----- 389  
 DB 329 TPMQALTNKDDNL-PRDSANATSLPVQDSSVPLPTFL-VAGSLAFGLLCLIAIVL 386  
 QY 390 ----LW-LRLRGGKDGSPKPGFLASVIPVDRRP 418  
 DB 387 RPKKTWKLKALKEGKTSMHPPYSIGQLVPERPRP 420  
 RESULT 7  
 IL6A\_PIG STANDARD; PRT; 467 AA.  
 ID IL6A\_PIG  
 AC O18796;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1).  
 GN IL6R.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]



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DR EMBL; M73238; AAA35707.1; -  
 DR EMBL; L38025; AAA91337.1; -  
 DR EMBL; L38023; AAA91337.1; JOINED.  
 DR EMBL; L38022; AAA91337.1; JOINED.  
 DR EMBL; L38024; AAA91337.1; JOINED.  
 DR PIR; A40854; UHUCN.  
 DR HSSP; P40189; LBQU.  
 DR MIM; I18946; -  
 DR InterPro; IPR000950; -  
 DR InterPro; IPR001777; -  
 DR InterPro; IPR002465; -  
 DR InterPro; IPR003006; -  
 DR Pfam; PF00041; fn3; 1.  
 DR Pfam; PF00047; fn3; 1.  
 DR PROSITE; PS01354; HEMATOPO\_REC\_L\_F3; 1.  
 KW Receptor; GPI-anchor; Glycoprotein; Immunoglobulin domain; Signal.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 342 CILIARY NEUROTROPHIC FACTOR RECEPTOR  
 FT PROPEP 343 372 REMOVED IN MATURE FORM (POTENTIAL).  
 FT DOMAIN 39 96 IG-LIKE C2-TYPE DOMAIN.  
 FT DISULFID 201 302 FIBRONECTIN TYPE-III.  
 FT POTENTIAL 46 89 POTENTIAL.  
 FT CARBOHYD 60 60 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 190 190 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT LIPID 342 342 GPI-ANCHOR (POTENTIAL).  
 SQ SEQUENCE 372 AA; 40633 MW; B2F3F73DE8F8750E CRC64;

Query Match 16.2%; Score 369.5; DB 1; Length 372;  
 Best Local Similarity 30.0%; Pred. No. 1.3e-18;  
 Matches 122; Conservative 47; Mismatches 168; Indels 69; Gaps 16;  
 QY 12 LVAVATALVSASSPCQAGPPGVQVQPGRSVKLCPCGVTAGDPVSVFRDGPFKLLQGP 71  
 DB 12 VLAATAAVVYQARSPQE--APHVQYERLGSVDVTLPCGTANMDAAVTRVNGTD---LAP 66  
 QY 72 DSGLGHSLVLAQADSDTEGYICQTLDG-ALGGTVTLQLCYPPARVVSQAADY-ENFS 129  
 DB 67 DLLNGSOLVHLGLELGHSGLYACFHRDSWHLRHQVLLHVLGPPREPVLSCRSNTYPKGY 126  
 QY 130 CTWSPSQISGLPT-RYLTYSYRKTIVLCADSQRRSPSTGWPCCPDPLGAARCVVHGAEEF 188  
 DB 127 CSWH-----LPTPTVITFNVTYVLSGSK-----IMVCEKDPALKNRCHIRYMHLF 172  
 QY 189 S--OYRINTEVNPGLGASTRLDLVLSQSLTRDPDQGLRVESVPGYRGLRASWTYPAS 246  
 DB 173 STIKYKVSISVSNALGNHNAITFOEF-TIVKDPDPNVVAVPSPNPRLEVTWTQTPST 231  
 QY 247 WPCQPHFLKFRQYPAQHPANSTVEPA-GLEEVITDAVAGLPHAVRVSAFDFLAGTW 305  
 DB 232 WPDPSFPLKFLFYRLPLIDQHQHVELSDGTAHTITDAYAGREYTIQVAAKD-NEIGTW 290  
 QY 306 STWSPAWGTPSTGTPKEIPANGQLHTQPEVPEQVDSAPPSPSLQHPRLDLDRHDSVE 365  
 DB 291 SDMSVAHAHATPTEE-PRHLLTTEAQ--AAETTTSTTSSLAAPP-----PTTKICD----- 336  
 QY 366 QVAVLASGLTSLGLVAGALALGLWLRLRRGGKDGSPKPGFLASV 411  
 DB 337 -----PGEL-----GSGGSPSAPFLVSV 354

RESULT 6  
 IL6A\_HUMAN  
 ID IL6A\_HUMAN STANDARD; PRT; 468 AA.

AC P08887; Q16202;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1)  
 DE (CD126 ANTIGEN).  
 GN IL6R.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (LONG ISOFORM).  
 RX MEDLINE=88305347; PubMed=3136546;  
 RA Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,  
 RA Taniguchi T., Hirano T., Kishimoto T.;  
 RT "Cloning and expression of the human interleukin-6 (BSF-2/IFN beta 2)  
 RT receptor.";  
 RL Science 241:825-828(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A. (LONG ISOFORM).  
 RA Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,  
 RA Taniguchi T., Hirano T., Kishimoto T.;  
 RT "Molecular structure of interleukin 6 receptor.";  
 RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 64:209-211(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A. (LONG ISOFORM).  
 RX MEDLINE=91336983; PubMed=1872801;  
 RA Schootlink H., Stoyan T., Lenz D., Schmitz H., Hirano T.,  
 RA Kishimoto T., Heinrich P.C., Rose-John S.;  
 RT "Structural and functional studies on the human hepatic interleukin-6  
 RT receptor. Molecular cloning and overexpression in HepG2 cells.";  
 RL Biochem. J. 277:659-664(1991).  
 RN [4]  
 RP SEQUENCE OF 313-365 FROM N.A. (SHORT ISOFORM).  
 RX MEDLINE=94333499; PubMed=8056053;  
 RA Horuchi S., Koyanagi Y., Zhou Y., Miyamoto H., Tanaka Y., Waki M.,  
 RA Matsumoto A., Yamamoto M., Yamamoto N.;  
 RT "Soluble interleukin-6 receptors released from T cell or  
 RT granulocyte/macrophage cell lines and human peripheral blood  
 RT mononuclear cells are generated through an alternative splicing  
 RT mechanism.";  
 RL Eur. J. Immunol. 24:1945-1948(1994).  
 RN [5]  
 RP PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.  
 RX MEDLINE=99167486; PubMed=10066782;  
 RA Cole A.R., Hall N.E., Treutlein H.R., Eddes J.S., Reid G.E.,  
 RA Moritz R.L., Simpson R.J.;  
 RT "Disulfide bond structure and N-glycosylation sites of the  
 RT extracellular domain of the human interleukin-6 receptor.";  
 RL J. Biol. Chem. 274:7207-7215(1999).  
 RN [6]  
 RP MUTAGENESIS.  
 RX MEDLINE=93223711; PubMed=8467812;  
 RA Yawata H., Yasukawa K., Natsuka S., Murakami M., Yamasaki K., Hibl M.,  
 RA Taga T., Kishimoto T.;  
 RT "Structure-function analysis of human IL-6 receptor: dissociation of  
 RT amino acid residues required for IL-6-binding and for IL-6 signal  
 RT transduction through gp130.";  
 RL EMBO J. 12:1705-1712(1993).  
 CC -!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6  
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL  
 CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY  
 CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE  
 CC REACTIONS AND HEMATOPOIESIS.  
 CC -!- FUNCTION: LOW CONCENTRATION OF A SOLUBLE FORM OF INTERLEUKIN-6  
 CC RECEPTOR ACTS AS AN AGONIST OF IL-6 ACTIVITY.  
 CC -!- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM) AND  
 CC SECRETED (SHORT FORM).  
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A  
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -!- TISSUE SPECIFICITY: THE SHORT FORM IS EXPRESSED IN PERIPHERAL



DE CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR (CNTFR ALPHA)  
DE (GROWTH PROMOTING ACTIVITY RECEPTOR ALPHA) (GPA RECEPTOR ALPHA) (GPAR  
DE ALPHA).  
GN CNTFR.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=96064819; PubMed=7595532;  
RA Ip F.C.F., Fu A.K.Y., Tsui K.W.K., Ip N.Y.;  
RT "Cloning of the alpha component of the chick ciliary neurotrophic  
RT factor receptor: developmental expression and down-regulation in  
RT denervated skeletal muscle."  
RL J. Neurochem. 65:2393-2400(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95401882; PubMed=7671828;  
RA Heller S., Finn T.P., Huber J., Nishi R., Geissen M., Pueschel A.W.,  
RA Rohrer H.;  
RT "Analysis of function and expression of the chick GPA receptor (GPAR  
RT alpha) suggests multiple roles in neuronal development."  
RL Development 121:2681-2693(1995).  
CC -!- FUNCTION: BINDS TO CNTF (GPA). THE ALPHA CHAIN PROVIDES THE  
CC RECEPTOR SPECIFICITY.  
CC -!- SUBUNIT: HETEROTRIMER OF THE ALPHA CHAIN, LIFR AND GP130.  
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY  
CC SIMILARITY).  
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN NERVOUS SYSTEM. ALSO FOUND  
CC IN SKELETAL MUSCLE.  
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -----  
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CC -----  
DR EMBL; U29245; AAA87838.1; -;  
DR EMBL; Z48168; CAA88184.1; -;  
DR HSP; P16471; IBP3.  
DR InterPro; IPR000950; -;  
DR InterPro; IPR001777; -;  
DR InterPro; IPR002465; -;  
DR InterPro; IPR003006; -;  
DR Pfam; PF00041; fn3; 1.  
DR Pfam; PF00047; 1g; 1.  
DR PROSITE; PS01354; HDMATOPO\_REC\_L\_F3; 1.  
KW Receptor; GPI-anchor; Glycoprotein; Immunoglobulin domain; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 334  
FT CILIARY NEUROTROPHIC FACTOR RECEPTOR  
FT ALPHA.  
FT PROPEP 335 362  
FT DOMAIN 37 94  
FT DOMAIN 199 300  
FT DISULFID 44 87  
FT CARBOHYD 58 58  
FT CARBOHYD 68 68  
FT CARBOHYD 140 140  
FT CARBOHYD 188 188  
FT LIPID 334 334  
FT CONFLICT 337 337  
FT SEQUENCE 362 AA; 40307 MW; 5A90217EB48419F7 CRC64;

Query Match

16.2%; Score 369.5; DB 1; Length 362;

Best Local Similarity 30.5%; Pred. No. 1.2e-18;  
Matches 120; Conservative 51; Mismatches 165; Indels 57; Gaps 17;  
Qy 2 SSSCSGLSRVLVAVATALVSASSPCQAWGPGVQYOGPRSVKLCPCGVTAGDPVSMFR 61  
Db 7 SACCVVLAADVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 57  
Qy 62 DGEPKLLOGDPSGL-GHELVLAQADSTDEGTYICOTLDGA---LGGTVTLQLGYPPARPV 117  
Db 58 NG----TDIDSHLNGSYLILKNVDLTQSGYSC--YEGSSWHLKYQTYLRVGVPPKEPV 111  
Qy 118 VSCQAADY-ENFSCWTS-PSQISGLPTRYLYTSYRKKTVLGADSQRRSPSTGFWPCQDPL 175  
Db 112 LMCRRNNYPKGYCSWHLPS-----PTVIPSFNISVTHG-----TREMWEKIDIF 157  
Qy 176 GAARCVVHGAFFWS--OYRINVTENVPLGGASTRLDVSLOSILRPPDQGLRVESVPGY 233  
Db 158 PKNRCHIRYLQFSTVKYKVTTLVTNALGKNSTTLTTFDEF-AIVAPDPPESSVAKPVNN 216  
Qy 234 PRGLRASWTYPASWPCQPHFLKFRLOYRPAQHPAWSTVEPA-GLEEVITDAVAGLPHAV 292  
Db 217 PRLVSHQNSWPPDPESFPLKFLRYRPLILDQWQHVLSGDTSHITDAYAGKEYII 276  
Qy 293 RVSARDFLDAGTWSPWSPWSTGTGTIPKEIPAWGQLHTQPEVEPQVDSAPPSPSLQ 352  
Db 277 QVAARD-NDIGTWSWVAVHATPWTEE-PKHLTT--EVQITETTTSTSTSSFMPP----- 327  
Qy 353 PHPRLLDHRDSVEQVA-----VLASLGIL 376  
Db 328 PTTKICDKAGVGSGAVAVCWTAGLVLAAYGVL 360  
RESULT 5  
ID CNTFR\_HUMAN STANDARD; PRT; 372 AA.  
AC P26992;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR (CNTFR ALPHA).  
GN CNTFR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91289158; PubMed=1648265;  
RA Davis S., Aldrich T.H., Valenzuela D.M., Wong V., Furth M.E.,  
RA Squinto S.P., Yancopoulos G.D.;  
RT "The receptor for ciliary neurotrophic factor."  
RL Science 253:59-63(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95293367; PubMed=7774913;  
RA Valenzuela D.M., Rojas E., le Beau M.M., Espinosa R.,  
RA Brannan C.I., McClain J., Masiakowski P., Ip N.Y., Copeland N.G.,  
RA Jenkins N.A., Yancopoulos G.D.;  
RT "Genomic organization and chromosomal localization of the human and  
RT mouse genes encoding the alpha receptor component for ciliary  
RT neurotrophic factor."  
RL Genomics 25:157-163(1995).  
CC -!- FUNCTION: BINDS TO CNTF (GPA). THE ALPHA CHAIN PROVIDES THE  
CC RECEPTOR SPECIFICITY.  
CC -!- SUBUNIT: HETEROTRIMER OF THE ALPHA CHAIN, LIFR AND GP130.  
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.  
CC -!- TISSUE SPECIFICITY: NERVOUS SYSTEM AND SKELETAL MUSCLE.  
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -----  
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QY 1 MSSCSGLSRVLVAVATYALVSASSPCQAWGPPGVYQGRSVKLCPCGVTAGD--PVS 58  
 Db 2 LAVGCTLLVALLAAPVALVLSG--CRALEAVANGTSLPGATVTLTLCGKEAAGNATIH 59  
 QY 59 WFRDGEPLKLOGPD-SGLGHELVLAQADSTDEGTYYICQTLGDLGALGCTVTLQGYPPARPV 117  
 Db 60 WYVSGS-----QSEWTTTNTLVRAVQNDTGHYLC-FLDDHLVGTVPFLLDVDPPEPK 114  
 QY 118 VSC-QAADYENFSCWSPSQISGLPTRYLTSYRKTKVLGADSORRSPSTGPPWPCP-QDPL 175  
 Db 115 LSCFRKNPLNFAECWHPSTPS-PTTKAVFAKKI-----NTNKGSDFOVPCQYSQOL 168  
 QY 176 GAARCVVHGAEFWSQVRI-NVTEVNPGLGASTRLDVSLSQSI--LRPDPQGLRVESVPG 232  
 Db 169 KSPCEVEILEGDKVYHIVSLCVANSVGRSSH--NVVFQSLKMVQDPDPPANLVSAIPG 226  
 QY 233 YPGLRASWTYPASWPCQPHLLKFLRYRPAQHAWMS-----TVEPAGLEE---VITDAVA 286  
 Db 227 XPRWLKVSQWODPESWD-PSYLLQFELRYR-----PWSKXFTVWPLQVAHQCVIHDALR 281  
 QY 287 GLPHAVRVSAARDPLDAGTWSTWSPWANGTPTCTIPKEIPAWGQLHTQPEVEPOVDSAP 346  
 Db 282 GYKHVVQVRGKEEFDIGQSKNSPEVTGTP-----W---LAEPRTTTPAGIPGNP 327  
 QY 347 PRPSLOPHRLDHRD-----SVEQVAVLA-----SLGILSFLGLVAGALGLW----- 391  
 Db 328 TVQSVSEVDYD---NHEDQYGSSTSEATSVLAPVQGSSTPIPLPTFL-VAGGSLAFGLLLCVFI 383  
 QY 392 -LRLRGGKD-----GSPKPGFLASVIVDRPRGAPN 422  
 Db 384 ILRLKKKKWSQAEKESKTTSPPPYPLGLPKPTFL--LVPLLTSPSGSHN 429

RESULT 3  
 CNTR\_RAT CNTR\_RAT STANDARD; PRT; 372 AA.

AC Q08406;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR (CNTRF ALPHA).  
 GN CNTRF.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=93152175; PubMed=8381290;  
 RA Ip N.Y., McClain J., Barzueeta N.X., Aldrich T.H., Pan L., Li Y.,  
 RA Wiegand S.J., Friedman B., Davis S., Yancopoulos G.D.;  
 RT "The alpha component of the CNTRF receptor is required for signaling  
 RT and defines potential CNTRF targets in the adult and during  
 RT development.";  
 RL Neuron 10:89-102(1993).  
 RN [2]  
 RP SEQUENCE OF 185-277 FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;  
 RX MEDLINE=93211934; PubMed=8460125;  
 RA Clatterbuck R.E., Price D.L., Koliatsos V.E.;  
 RT "Ciliary neurotrophic factor prevents retrograde neuronal death in  
 RT the adult central nervous system.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2222-2226(1993).  
 CC -!- FUNCTION: BINDS TO CNTRF (GPA). THE ALPHA CHAIN PROVIDES THE  
 CC RECEPTOR SPECIFICITY.  
 CC -!- SUBUNIT: HETEROTRIMER OF THE ALPHA CHAIN, LIFR AND GPI30.  
 CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.  
 CC -!- TISSUE SPECIFICITY: NERVOUS SYSTEM.  
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: S54212; AAB25290.1; -  
 DR EMBL: S57711; AAB25918.1; -  
 DR PIR: A47387; A47387.  
 DR InterPro: IPR000950; -  
 DR InterPro: IPR001777; -  
 DR InterPro: IPR002465; -  
 DR InterPro: IPR003006; -  
 DR Pfam: PF00041; f03; 1.  
 DR Pfam: PF00047; f03; 1.  
 DR PROSITE: PS01354; HEMATOPO\_REC\_L\_F3; 1.  
 KW Receptor; GPI-anchor; Glycoprotein; Immunoglobulin domain; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 342  
 FT ALPHA  
 FT PROPEP 343 372  
 FT DOMAIN 39 96  
 FT DOMAIN 201 302  
 FT DISULFID 46 89.  
 FT CARBOHYD 60 60  
 FT CARBOHYD 70 70  
 FT CARBOHYD 142 142  
 FT CARBOHYD 190 190  
 FT CARBOHYD 261 261  
 FT LIPID 342 342  
 FT CONFLICT 261 261  
 FT SEQUENCE 372 AA; 40822 MW; 3B87EE63923FB149 CRC64;  
 N -> D (IN REF. 2).  
 Query Match 16.4%; Score 374.5; DB 1; Length 372;  
 Best Local Similarity 31.5%; Pred. No. 5.8e-19;  
 Matches 112; Conservative 49; Mismatches 165; Indels 29; Gaps 13;  
 QY 1 MSSCSGLSRVLVAVATYALVSASSPCQAWGPPGVYQGRSVKLCPCGVTAGDPSVWF 60  
 Db 1 MAASVPWACCAVLAALAAAAAAYTKHSPQE--APHVQYERLGTDTVLPCGTASWDAAVTWR 58  
 QY 61 RDCEPKLLQGGPSGLGHELVLAQADSTDEGTYYICQTLGDLG-ALGGTVTTLQGYPPARPVVS 119  
 Db 59 VNGTD---LAPDLLNGSLILSLSLGSLGACFHRDSHLRHQVLLHVLGLPPREPVL 115  
 QY 120 QCAADY-ENFSCWSPSQISGLPTRYLTSYRKTKVLGADSORRSPSTGPPWPCQDPLGAA 178  
 Db 116 CRSNTYKGYFCWSHLS---APT-YIPNTFNTVLHGSKN-----MVCEKDPALKN 162  
 QY 179 RCVVHGAEFWS--OYRINTVENPLGCASTRLLDVSLSQSI--LRPDPQGLRVESVPGYPRG 236  
 Db 163 RCHIRYMHLEFTIKYKVSISVSNAL-GHNTTATTFDEFTIKVDPDPENVVAVRVPSPNRR 221  
 QY 237 LRASWTYPASWPCQPHLLKFLRYRPAQHAWMSVTEPA-GLEEVITDAVAGLPHAVRVS 295  
 Db 222 LEVWTQTPSTWPDPESEPLKFFLYRPLLDQWQHVSLSNGTAHTITDAYAGKEYLIQVA 281  
 QY 296 ARDLFDAGTWSTWSPWANGTPTCTIPKEIPAWGQLHTQPEVEPOVDSAPPPT 350  
 Db 282 AKD-NEIGTWSQWSDVAHAATPWTEE-PRHLTTEAQ---APETTTTSSSLAPPPT 331  
 RESULT 4  
 CNTR\_CHICK  
 ID CNTR\_CHICK STANDARD; PRT; 362 AA.  
 AC P51541;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DR MGD; MGI:105304; IL6ra.  
DR InterPro; IPR000950; -  
DR InterPro; IPR001777; -  
DR InterPro; IPR002465; -  
DR InterPro; IPR003006; -  
DR Pfam; PF00041; fn3; 1.  
DR Pfam; PF00047; ig; 1.  
DR PROSITE; PS01354; HEMATOPO\_REC\_L\_F3; 1.  
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;  
KW Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 460 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.  
FT DOMAIN 20 364 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 365 385 POTENTIAL.  
FT DOMAIN 386 460 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 40 99 IG-LIKE C2-TYPE DOMAIN.  
FT DISULFID 25 190 BY SIMILARITY.  
FT DISULFID 47 92 BY SIMILARITY.  
FT DISULFID 117 128 BY SIMILARITY.  
FT DISULFID 162 173 BY SIMILARITY.  
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 374 374 A -> R (IN REF. 2).  
SQ SEQUENCE 460 AA; 50454 MW; F85C5906D08525C4 CRC64;

Query Match 17.68; Score 402; DB 1; Length 460;  
Best Local Similarity 30.68; Pred. No. 9.5e-21;  
Matches 144; Conservative 55; Mismatches 184; Indels 88; Gaps 23;

OY 1 MSSCSGLSRVLAVATVALVSASSPCQAGPPGQVQYQGRSVKLCPCGTAGDPVS-- 58  
DB 2 LTVGCTLLVALLAFAVALVLS--CRALEVANGVTSLPGATVTLICPGKEAGNVTIH 59  
OY 59 WFRDGEKLLGPD--SGLGHELVLAQADSTEGYICOTLGLAGGVTVTLQGVPPARPV 117  
DB 60 WYSGS----QNREWTGNTLVLRDVLQSDTGDIYC--SLNDHLVLTPLVLDVPPPEPK 114  
OY 118 VSC-QAADYENFSCWSPQISGLPLTRVLTYSRKTVLGDADRSPTSGWPWCQ-QDPL 175  
DB 115 LSCFRKPLVNAICWSPSTPS-PTTKAVLFARKI-----NTNGKSDFOVPCQYSOOL 168  
OY 176 GAARCVHGAFFWSQYRI--NVTENPLGGASTRLLDLSQSLRDPDPPQGLRVESVPGYP 234  
DB 169 KSFSCQVEILEGDKYHIVSLCVANSVGSKSHNEAFHSLKMWQDPPANLVWSAIPGRP 228  
OY 235 RGLRASWTYPASWPCQPHFLKFRQYRPAQHPAWS-----TVEPAGLEEIVTDAVAGL 288  
DB 229 RMLKVSWQHPTWD--PSYLLQFQLRYR----PVWSKEFTVLLLPVAQYQCVIHDALRGV 283  
OY 289 PHAVRVSRDFLDAGTWSTPEANGTPTGTIPKEIPA---WGOLHTQPEVEPOVDSPA 345  
DB 284 KHVVQVRKEELDQGWSEWSPVETGTWIAE-PRTTAGILWNP--TQVSVSE---DS-- 335  
OY 346 PPRPSLOPHRLLDHRD----SVEQAVLA-----SIGILSFLGLVAGALGLW---- 391  
DB 336 -----ANHEDQVESSTATSVLAPVQESSSSSLPTFL-VAGSLAFGLLLCVF 382  
OY 392 --LRURRGKD-----GSPKPGFLASVIVDVRGAPN 422  
DB 383 IILRLKQWKSEAEKESKTPPPPPYSLGPLKPTFLVLLPLTLTHSSGSDN 433

RESULT 2  
IL6A\_RAT  
ID IL6A\_RAT STANDARD; PRT; 462 AA.  
AC P22273;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1).  
GN IL6R.

OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-FISCHER 344; TISSUE=Liver;  
RX MEDLINE=91060602; PubMed=2174054;  
RA Baumann M., Baumann H., Fey G.H.;  
RT "Molecular cloning, characterization and functional expression of the  
rat liver interleukin 6 receptor.";  
RL J. Biol. Chem. 265:19853-19862(1990).  
RN [2]  
RP IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.  
RA Gibson T.;  
CC Unpublished observations (FEB-1995).  
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6  
WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL  
ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY  
LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE  
REACTIONS AND HEMATOPOIESIS.  
CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY  
SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE  
C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
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or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC  
CC EMBL; M58587; AAA41431.1; -  
CC PIR; A37986; A37986.  
CC HSP; P16471; IBP3.  
DR InterPro; IPR000950; -  
DR InterPro; IPR001777; -  
DR InterPro; IPR002465; -  
DR Pfam; PF00041; fn3; 1.  
DR Pfam; PF00047; ig; 1.  
DR PROSITE; PS01354; HEMATOPO\_REC\_L\_F3; 1.  
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;  
KW SIGNAL.  
FT SIGNAL 1 19  
FT CHAIN 20 462 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.  
FT DOMAIN 20 364 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 365 385 POTENTIAL.  
FT DOMAIN 386 462 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 40 99 IG-LIKE C2-TYPE DOMAIN.  
FT DISULFID 25 190 BY SIMILARITY.  
FT DISULFID 47 92 BY SIMILARITY.  
FT DISULFID 117 128 BY SIMILARITY.  
FT DISULFID 162 173 BY SIMILARITY.  
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 227 261 XPRWLKVSQDPESDPFVSYLQELRYPVWSX ->  
SLVGSVSGKTLSPGTQVTTCCNSFDTDLVGQRT  
(IN REF. 1).  
SQ SEQUENCE 462 AA; 50398 MW; A4D6064CEDC0537D CRC64;

Query Match 17.48; Score 398; DB 1; Length 462;  
Best Local Similarity 30.8%; Pred. No. 1.8e-20;  
Matches 144; Conservative 56; Mismatches 182; Indels 86; Gaps 25;

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 24, 2001, 17:34:32 ; Search time 15.19 Seconds  
(without alignments)  
953.922 Million cell updates/sec

Title: US-09-532-263-5

Perfect score: 2282

Sequence: 1 MSSSCSGLSRVLVAVATALV.....KPGFLASVIPVDRRPGAPNL 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	402	17.6	460	1	IL6A_MOUSE	P22272 mus musculus
2	398	17.4	462	1	IL6A_RAT	P22273 rattus norv
3	374.5	16.4	372	1	CNTR_RAT	Q08406 rattus norv
4	369.5	16.2	362	1	CNTR_CHICK	P51641 gallus gall
5	369.5	16.2	372	1	CNTR_HUMAN	P08992 homo sapien
6	367.5	16.1	468	1	IL6A_HUMAN	P08887 homo sapien
7	336	14.7	467	1	IL6A_PIG	O18796 sus scrofa
8	236.5	10.4	831	1	PRIR_MELGA	Q91094 meleagris g
9	222.5	9.8	830	1	PRIR_COLLI	Q90374 columba liv
10	216.5	9.5	831	1	PRIR_CHICK	Q04594 gallus gall
11	207	9.1	581	1	PRIR_BOVIN	Q28172 bos taurus
12	201	8.8	581	1	PRIR_CEREL	Q28235 cervus elap
13	195.5	8.6	616	1	PRIR_RABIT	P14787 oryctolagus
14	191.5	8.4	610	1	PRIR_RAT	P05710 rattus norv
15	189.5	8.3	622	1	PRIR_HUMAN	P16471 homo sapien
16	183.5	8.0	327	1	I12B_CAPHI	O18989 capra hircu
17	183.5	8.0	1266	1	NGCA_CHICK	Q03696 gallus gall
18	181.5	8.0	327	1	I12B_MARMO	Q61729 marmota mon
19	180	7.9	630	1	PRIR_ORENI	Q91513 oreochromis
20	179.5	7.9	327	1	I12B_BOVIN	P46282 bos taurus
21	175.5	7.7	327	1	I12B_CEREL	Q28234 cervus elap
22	175.5	7.7	608	1	PRIR_MOUSE	Q08501 mus musculus
23	171	7.5	324	1	I12B_PIG	Q28938 sus scrofa
24	167	7.3	329	1	I12B_FELCA	Q02744 felis silve
25	165	7.2	761	1	NCAL_HUMAN	P13592 homo sapien
26	163.5	7.2	327	1	I12B_SHEEP	O02815 ovis aries
27	163	7.1	328	1	I12B_MACMU	P48095 macaca mula
28	160	7.0	328	1	I12B_HUMAN	P29460 homo sapien
29	155.5	6.8	918	1	IL6B_HUMAN	P40189 homo sapien
30	154.5	6.8	329	1	I12B_HORSE	Q9X8Q5 equus caball
31	149.5	6.6	836	1	GCSR_HUMAN	Q99062 homo sapien
32	148	6.5	853	1	NCAL_BOVIN	P18183 bos taurus
33	146	6.4	917	1	IL6B_MOUSE	Q00560 mus musculus

34	145	6.4	328	1	I12B_CERTO	P45658 cercocebus
35	145	6.4	858	1	NCAL_RAT	P13596 rattus norv
36	144	6.3	329	1	I12B_CANFA	Q28268 canis famil
37	144	6.3	848	1	NCAL_HUMAN	P13591 homo sapien
38	141	6.2	1162	1	LEPR_MOUSE	P48356 mus musculus
39	140	6.1	1897	1	PTPF_HUMAN	P10586 homo sapien
40	138.5	6.1	335	1	I12B_MOUSE	P43432 mus musculus
41	138	6.0	890	1	TYO3_HUMAN	Q08418 homo sapien
42	138	6.0	1092	1	LIFR_MOUSE	P42703 mus musculus
43	134.5	5.9	297	1	GHRH_MOUSE	P16590 mus musculus
44	134.5	5.9	650	1	GHRH_MOUSE	P16882 mus musculus
45	133.5	5.9	638	1	GHR_RAT	P16310 rattus norv

#### ALIGNMENTS

RESULT 1  
ID IL6A\_MOUSE STANDARD; PRT: 460 AA.  
AC P22272;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (IL-6R 1).  
GN IL6RA OR IL6R.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C; TISSUE=Spleen;  
RX MEDLINE=90278354; PubMed=2112585;  
RA Sugita T., Totsuka T., Saito M., Yamasaki K., Taga T., Hirano T.,  
RA Kishimoto T.;  
RT "Functional murine interleukin 6 receptor with the intracisternal A  
particle gene product at its cytoplasmic domain. Its possible role in  
plasmacytogenesis.";  
RT J. Exp. Med. 171:2001-2009(1990).  
RL [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=C3H; TISSUE=Liver;  
RC Fiorillo M.T., Ciliberto G., Dente L.;  
RA Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.  
RL  
CC 1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6  
WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL  
ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY  
LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE  
REACTIONS AND HEMATOPOIESIS.  
CC 1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY  
SIMILARITY).  
CC 1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC 1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE  
C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.  
CC 1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
CC 1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC 1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC  
CC EMBL; X51975; CAA36237.1; .  
CC EMBL; X53802; CAA37810.1; .  
DR PIR; JLO144; JLO144.  
DR PIR; JLO145; JLO145.  
DR PIR; S14543; S14543.  
DR HSP; P16471; IBP3.  
DR

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.QY 339 ---PQVDSAPPRPSLQPHPRLLDHRDSVEQV 367

F:36-221/Domain: cytokine receptor homology <CRS>

A:Reference number: A40854; MUID:91289158  
A:Accession: A40854  
A:Molecule type: mRNA  
A:Residues: 1-372 <DAV>  
A:Cross-references: GB:M73238  
R:Valenzuela, D.M.; Rojas, E.; Le Beau, M.M.; Espinosa III, R.; Brannan, C.L.; McClain, Genomics 25, 157-163, 1995  
A:Title: Genomic organization and chromosomal localization of the human and mouse genes  
A:Reference number: A56526; MUID:95293367  
A:Accession: A56526  
A:Molecule type: DNA  
A:Residues: 1-346, S', 348-372 <VAL>  
A:Cross-references: GB:L38025; NID:9608654; PIDN:AAA91337.1; PID:9608656  
C:Comment: The CNTF receptor is attached to the membrane by a glycosylphosphatidylinositol  
C:Comment: The CNTF receptor sequence appears to contain several PEST regions.  
C:Genetics:  
A:Gene: GDB:CNTRF  
A:Cross-references: GDB:134652; OMIM:118946  
A:Map position: 9p13-9p13  
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; Immunoglobulin-like domain; growth factor receptor; membrane protein; phosphatidylinositol  
F:1-372/Domain: signal sequence #status predicted <SIG>  
F:21-372/Product: ciliary neurotrophic factor receptor #status predicted <MAT>  
F:39-91/Domain: immunoglobulin homology <IMM>  
F:116-296/Domain: cytokine receptor homology <CRS>  
F:46-89/disulfide bonds: #status predicted  
F:60,70,142,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.1%; Score 366.5; DB 1; Length 372;  
Best Local Similarity 30.0%; Pred. No. 4.1e-17;  
Matches 122; Conservative 47; Mismatches 168; Indels 69; Gaps 16;

QY 12 LVAVATALVSASSPCQAWPGVQVQGPGRSVKLCPCGTAGDPVSVFRDGPCKLQGP 71  
DB 12 VLAARAAVYAQRHSQEE--APHVQVERLGSDVTLPCGTANWDAATVWRVNGTD---LAP 66  
QY 72 DSGLGHVLAQADSTDEGTYICQTLDG-ALGCTVTLOLGYPPARPVSCAAADY-ENFS 129  
DB 67 DLLNGSQLVHLGLHSGLYACFRHSDWHLRHQVLLHVLGPPREPVLSCRSNTYPKGFY 126  
QY 130 CTWSPSQISGLPT-RVLTYSRKTKTVLCADSORSPSTGWPCCQDPLGCAACVHVGAEFW 188  
DB 127 CSMW-----LPTPTIPNTFNFTVHLGSK-----IMVCEKDPALKNRCHIRYMHLF 172  
QY 189 S--QYRINVTENPLGASRTRLDVLSQILRDPDPOGLRVESVPGYPRGLRASWTYPAS 246  
DB 173 STIKYKVISVSNALGHNAATATFDEF-TIVKDPDENVVARVPVSNPRRLEVTWQTPST 231  
QY 247 WPCQPHFLKFRQYRPAQHPANSTVEPA-GLEEVITDAVAGLPHAVRVASARDFLDAGTW 305  
DB 232 WPDPSFPLKFFLYRPLLDQHVLSLSDGTAHTITDAYAGREYITQVAAKD-NEIGTW 290  
QY 306 STWSPKAWGTPGTGTPKEIPANGQLHTQPEVQVDSAPPSPLOPHRLDHRDSEV 365  
DB 291 SDWSVAHAHATPTEE-PRUUTTEAQ--AAETTTSTTSSLAPP-----PTTKICD----- 336  
QY 366 QVAVLASGLTSLGLVAGALALGLWLRRLRGCKGDSRKPGLASV 411  
DB 337 -----PGEL-----GSGGGPCAPFLVSV 354

RESULT 9  
A37986  
Interleukin-6 receptor precursor - rat  
N:Alternate names: IL-6 receptor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #Text\_change 22-Jun-1999  
A:Accession: A37986  
R:Baumann, M.; Baumann, H.; Fey, G.H.  
J. Biol. Chem. 265, 19853-19862, 1990  
A:Title: Molecular cloning, characterization and functional expression of the rat liver  
A:Reference number: A37986; MUID:91060602

A:Accession: A37986  
A:Molecule type: mRNA  
A:Residues: 1-462 <BAU>  
A:Cross-references: GB:M58587; GB:J05668; NID:9204921; PIDN:AAA41431.1; PID:9204922  
C:Comment: After binding IL-6, this chain associates with a 130K glycoprotein that is  
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; Immunoglobulin-like domain; growth factor receptor; membrane protein  
F:1-462/Domain: signal sequence #status predicted <SIG>  
F:20-462/Product: Interleukin-6 receptor #status predicted <MAT>  
F:20-362/Domain: extracellular #status predicted <EXT>  
F:40-94/Domain: immunoglobulin homology <IMM>  
F:117-306/Domain: cytokine receptor homology <CRS>  
F:363-385/Domain: transmembrane #status predicted <TM>  
F:386-462/Domain: intracellular #status predicted <INT>  
F:47-92/disulfide bonds: #status predicted

Query Match 13.4%; Score 306; DB 1; Length 462;  
Best Local Similarity 27.1%; Pred. No. 4.9e-13;  
Matches 132; Conservative 51; Mismatches 180; Indels 124; Gaps 25;

QY 1 MSSSCSGLSRVLVAVATALVSASSPCQAWPGVQVQGPGRSVKLCPCGTAGD--PVS 58  
DB 2 LAVGCTLLVALLAAPVALVLGS--CRALEVANGTVTSLPATVTLICPKKEAGNATHI 59  
QY 59 WFRDGPCKLQGPD-SGLGHVLAQADSTDEGTYICQTLDGALGCTVTLOLGYPPARPV 117  
DB 60 WYVSGS----QSRWTTTNTLVRAVQVNDTGHYLC-FLDDHVLGVTVPLLDVDPPEPK 114  
QY 118 VSC-QAADYENFSCVTSQISGLPTRYLTYSRKTKTVLCADSORSPSTGWPCCP-QDPL 175  
DB 115 LSCFRKNPLVNAFCEWHPSSTPS-PTTKAVMFAKKI-----NTTNGKSDQVPCQYSQOL 168  
QY 176 GAARCVVHGAEFWSQYRI-NVTEVNPLGGASTRLDVLSQSI--LRPDPQGLRVESVPG 232  
DB 169 KSPCEVEILEGDKVTHIVSLCVANSVSGSRSH--NVVFQSLKMWQDPPANLVVSAIPG 226  
QY 233 -----YPRGLRASWTYPASWPCQPHFLKFRQYRPAQHP 267  
DB 227 SLVGSKSVGKTLSPGTQVTTCCNSSEFDTLYGQRTFTV-WPLQ-----VAHQH 273  
QY 268 AMSTVEPAGLEEVITDAVAGLPHAVRVASARDFLDAGTWISWSPANGTPTGTIPKEIPA 327  
DB 274 C-----VIHDALRGVHVQVRGKEEDFDIGQWSKWSPEVTGTP----- 311  
QY 328 WQQLHTQPEVQVDSAPPSPLOPHRLDHRD-----SVEQVAVLA-----SLGILS 377  
DB 312 W---LAEPRTTAPAGIPGNTOVSVEYD---NHEDQYGSSTEATSVLAPVQGSPIPLPT 365  
QY 378 FLGLVAGALALGLW-----LRLRRGGKD-----GSPKPGFLASVIPVD 415  
DB 366 FL-VAGSGLAFGLLLCVFIILRLKKWKSQAEKSTTSPPPYPLGLPKPTFL--LVPLL 422  
QY 416 RRPQAPN 422  
DB 423 TPGSGSHN 429

RESULT 10  
I50455  
prolactin receptor - pigeon  
C:Species: Columba livia (domestic pigeon)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1995 #text\_change 28-Jul-2000  
C:Accession: I50455  
R:Chen, X.; Horseman, N.D.  
Endocrinology 135, 269-276, 1994  
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor  
A:Reference number: I50455; MUID:94283367  
A:Accession: I50455  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-830 <CHE>  
A:Cross-references: EMBL:U07694; NID:g466381; PIDN:AAA20646.1; PID:g466382





Db 229 RWLKVSNQHPETWD-PSYLLQQLRYR-----PWSKEFTVLLPVAQYQCVIHDLRGV 283  
QY 289 PHAVRYSARDFLDAGTWSTWSPAWGTPTGTIPKEIPA---WGQLHTQPEVPEQVDSPA 345  
Db 284 KHVVQVQKREELDQGWSEWSPVETGTPWIAE-PRITPAGILWNP--TQVSV-----DS-- 335  
QY 346 PPRPSLOPHRLDHRD-----SVEQVAVLA-----SLGILSLGLVAGALGLW---- 391  
Db 336 -----ANHEDQESSTEATSVLAPVQESSMSLPTFL-VAGGSLAFGLLLCVF 382  
QY 392 --LRLRRGGKD-----GSPKPGFLASVIPVDRRGPAPN 422  
Db 383 IILRLKQKWEAKESKSTSPPPPPYSLGPKLPTLLVPLTPHSSGSDN 433  
RESULT 4  
JL0144  
Interleukin-6 receptor precursor (clone lambda Pl) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 21-Jan-2000  
C:Accession: JL0144  
R:Sugita, T.; Totsuba, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.  
J. Exp. Med. 171, 2001-2009, 1990  
A:Title: Functional murine interleukin 6 receptor with the intracisternal a particle gene  
A:Reference number: JL0144; MUID:90278354  
A:Accession: JL0144  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-440 <SUG>  
A:Cross-references: GB:X51976; NID:953548; PIDN:CAA36238.1; PID:953549  
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; Immunoglobulin  
C:Keywords: cytokine receptor; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-440/Product: interleukin-6 receptor #status predicted <MAT>  
F:40-94/Domain: immunoglobulin homology <IMM>  
F:117-306/Domain: cytokine receptor homology <CRS>  
F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match 17.4%; Score 396; DB 2; Length 440;  
Best Local Similarity 32.1%; Pred. No. 5.6e-19;  
Matches 134; Conservative 51; Mismatches 168; Indels 64; Gaps 21;  
QY 1 MSSCSGLSRVLVAVATLVASASSPCQAWPGVQYQGPGRSVKLCPCCVTAGDPVSV-- 58  
Db 2 LTGVTCLLVALLAAPAVALVLSG--CRALEVANGTVTSLPGAIVTLICPKKEAGNVTH 59  
QY 59 WFRDGPKLQGGD--SGLGHVLAQADSTDEGTTCQILDGALGCTVTLQGLYPPARPV 117  
Db 60 WYVSGS---QNRWTTTNTLVRLDVQLSDTDGYLC--SLNDHLVGTVPVLLVDVPEERK 114  
QY 118 VSG-QAADYENFSCWSPSQISGLPTRYLTSYRKYTKVLGADSORRSPSTGCPWPCP-QDPL 175  
Db 115 LSCFRNLVNAICENRPSSTPS-PTTKAVLFAKKI-----NTNGKSDQVPCQYSQQL 168  
QY 176 GAARCVVHGAEFWSQYRI-NVTEVNPGLGASTRLDLVLSQSLRPPDPQGLRVESVPGYP 234  
Db 169 KPSFCQVEILEGDKVHYVLSLVANSVSGSKSHNEAFSLKWKVQDPDPANLVVSAIPGRP 228  
QY 235 RGLRASWTYPASWPCQPHFLKFRLOYRPAQHPAWS-----TVEPAGLEEVTIDAVAGL 288  
Db 229 RWLKVSNQHPETWD-PSYLLQQLRYR-----PWSKEFTVLLPVAQYQCVIHDLRGV 283  
QY 289 PHAVRYSARDFLDAGTWSTWSPAWGTPTGTIPKEIPA---WGQLHTQPEVPEQVDSPA 345  
Db 284 KHVVQVQKREELDQGWSEWSPVETGTPWIAE-PRITPAGILWNP--TQVSV-----DS-- 335  
QY 346 PPRPSLOPHRLDHRD-----SVEQVAVLA-----SLGILSLGLVAGALGLW---- 392  
Db 336 -----ANHEDQESSTEATSVLAPVQESSMSLPTFL-VAGGSLAFGLLL 379

RESULT 5  
I58141  
ciliary neurotrophic factor receptor alpha chain - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 23-Jul-1999  
C:Accession: I58141; A47387  
R:Ip, N.Y.; McClain, J.; Barrezaeta, N.X.; Aldrich, T.H.; Pan, L.; Li, Y.; Wiegand, S.  
Neuron 10, 89-102, 1993  
A:Title: The alpha component of the CNTF receptor is required for signaling and defin  
A:Reference number: I58141; MUID:93152175  
A:Accession: I58141  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-372 <IPN>  
A:Cross-references: GB:S54212; NID:g265055; PIDN:AAB25290.1; PID:g265056  
R:Clatterbuck, R.E.; Price, D.L.; Koliatsos, V.E.  
Proc. Natl. Acad. Sci. U.S.A. 90, 2222-2226, 1993  
A:Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult  
A:Reference number: A47387; MUID:93211934  
A:Accession: A47387  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 185-260, 'D', 262-277 <CLA>  
A:Cross-references: GB:S57711; NID:g299331; PIDN:AAB25918.1; PID:g299332  
A:Experimental source: Sprague-Dawley, brain  
A:Note: sequence extracted from NCBI backbone (NCBI:128471, NCBIP:128472)  
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu  
C:Keywords: growth factor receptor  
F:39-91/Domain: immunoglobulin homology <IMM>  
F:116-296/Domain: cytokine receptor homology <CRS>  
Query Match 16.4%; Score 374.5; DB 2; Length 372;  
Best Local Similarity 31.5%; Pred. No. 1.2e-17;  
Matches 112; Conservative 49; Mismatches 165; Indels 29; Gaps 13;  
QY 1 MSSCSGLSRVLVAVATLVASASSPCQAWPGVQYQGPGRSVKLCPCCVTAGDPVSWF 60  
Db 1 MAASVPWACCVALAAAAAVYTKHSPQE--APHVQVERIGTDTVTLPCGTASMDAAVTWR 58  
QY 61 RDEPKLQGGD--SGLGHVLAQADSTDEGTTCQILDG--ALGTVTLQGLYPPARPVVS 119  
Db 59 VNGTD---LAPDLNGSLQLTLRLSLGLSYACFHRDMSHLRHQLLVHGLPLPREVLS 115  
QY 120 QAAADY-ENFSCWSPSQISGLPTRYLTSYRKYTKVLGADSORRSPSTGCPWPCQDPLGAA 178  
Db 116 CRNTYKPGFYCSWHLN---APT-YIPNTFNTVTLNGSKM-----MVCEKDPALKN 162  
QY 179 RCVVHGAEFWS---QYRINVTENVPLGGASTRLDLVLSQSLRPPDPQGLRVESVPGYPGR 236  
Db 163 RCHIRYMHFLFTIKYKVSISVSNAL-GHNTTAITDEFDEFTVKKPDPENNVARVPVSNPRR 221  
QY 237 LRASWTYPASWPCQPHFLKFRLOYRPAQHPAWSVEPA-GLEEVITDAVAGLPHAVRVS 295  
Db 222 LEVWTQTPSTWPDPEFPLKFFLRYRPLDLDQWQHVLSNGTARTITDAYAGKEYIIQVA 281  
QY 296 ARDFLDAGTWSTWSPAWGTPTGTIPKEIPAWQLHTQPEVPEQVDSPPAPRPS 350  
Db 282 AKD-NEIGTWSWDSVAHAHATPWTEE-PRHLTTEAQ---APETTTSTTSSLAPPT 331  
RESULT 6  
S60614  
growth promoting activity receptor alpha precursor - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 21-Jul-2000  
C:Accession: S60614  
R:Heller, S.; Finn, T.P.; Huber, J.; Nishi, R.; Geissen, M.; Pueschel, A.W.; Rohrer,  
Development 121, 2681-2693, 1995  
A:Title: Analysis of function and expression of the chick GPA receptor (GPalpha) su  
A:Reference number: S60614; MUID:95401882  
A:Accession: S60614  
A:Status: preliminary; nucleic acid sequence not shown

QY 181 VVHGAFFWSQYRINVTENVPLGGASTRLLDVSLQSLRPDPQGLRVSVPGYPRGLRAS 240  
DB 181 VVHGAFFWSQYRINVTENVPL--GASTRLLDVSLQSLRPDPQGLRVSVPGYPRGLRAS 239

QY 241 WTYPASWPCQPHFLKFRLOYRPAQHAWSTVEPAGLVEVITDAVAGLPHAVRVVSARDFL 300  
DB 240 WTYPASWPCQPHFLKFRLOYRPAQHAWSTVEPAGLVEVITDAVAGLPHAVRVVSARDFL 299

QY 301 DAGTWTSTWSPAWGTPTGTIPKEIPANGQLHTQ--PEVEQVDSPPAPRPSLQHPRLLDH 360  
DB 300 DAGTWTSTWSPAWGTPTGTIPKEIPANGQLHTQ--PEVEQVDSPPAPRPSLQHPRLLDH 299

QY 361 RDSVEQVAVLASLGLSFLGLVAGALGLMLRLRRGKDGSPKPGFLASVIPPVDRRPGA 420  
DB 360 RDSVEQVAVLASLGLSFLGLVAGALGLMLRLRRGKDGSPKPGFLASVIPPVDRRPGA 419

QY 421 PNL 423  
DB 420 PNL 422

RESULT 2  
148343  
Interleukin-11 receptor alpha-chain precursor - mouse  
N:Alternate names: cytokine type 1 receptor  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 31-Jan-2000  
C:Accession: I48343; S51619  
R:Neuhaus, H.; Bettenhausen, B.; Billinski, P.; Simon-Chazottes, D.; Guenet, J.L.; Gossle  
Dev. Biol. 166, 521-542, 1994  
A:Title: et12, a novel putative type-1 cytokine receptor expressed during mouse embryoge  
A:Reference number: 148343  
A:Accession: I48343  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-432 <RES>  
A:Cross-references: EMBL:X74953; NID:G673437; PIDN:CAA52908.1; PID:G673438  
R:Hilton, D.J.; Hilton, A.A.; Raicevic, A.; Rakar, S.; Harrison-Smith, M.; Gough, N.M.;  
EMBO J. 13, 4765-4775, 1994  
A:Title: Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130 for high  
A:Reference number: S51619; MUID:95045367  
A:Accession: S51619  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-432 <HIL>  
A:Cross-references: EMBL:U14412; NID:G576454; PIDN:AAA53248.1; PID:G576455  
C:Genetics:  
A:Gene: Et12/Il11  
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog  
C:Keywords: cytokine receptor  
F:120-310/Domain: cytokine receptor homology <CRS>

QY 1 1MSSCSGLSRLVAVATALVSASSPCQAWGPPGYOGPGRSVKLCPCGVTAGDPVSWF 60  
DB 1 1MSSCSGLSRLVAVATALVSASSPCQAWGPPGYOGPGRSVKLCPCGVTAGDPVSWF 60

QY 61 RDGEPKLLQGDPSGLGHELVLAQADSTDEGTYICOTLDGALGGTTLQGLYPPARPVSC 120  
DB 61 RDGSRLLQGDPSGLGHELVLAQADSTDEGTYICOTLDGALGGTTLQGLYPPARPVSC 120

QY 121 QAADYENFSCWSPSQISGLPTRYLTSYRKKTIVLGADSQRRSPSPGWPCCPDPLGAARC 180  
DB 121 QAADYENFSCWSPSQISGLPTRYLTSYRKKTIVLGADSQRRSPSPGWPCCPDPLGAARC 180

QY 181 VVHGAFFWSQYRINVTENVPLGGASTRLLDVSLQSLRPDPQGLRVSVPGYPRGLRAS 240  
DB 181 VVHGAFFWSQYRINVTENVPL--GASTRLLDVSLQSLRPDPQGLRVSVPGYPRGLRAS 239

QY 241 WTYPASWPCQPHFLKFRLOYRPAQHAWSTVEPAGLVEVITDAVAGLPHAVRVVSARDFL 300  
DB 240 WTYPASWPCQPHFLKFRLOYRPAQHAWSTVEPAGLVEVITDAVAGLPHAVRVVSARDFL 299

QY 301 DAGTWTSTWSPAWGTPTGTIPKEIPANGQLHTQ--PEVEQVDSPPAPRPSLQHPRLLDH 358  
DB 300 DAGTWTSTWSPAWGTPTGTIPKEIPANGQLHTQ--PEVEQVDSPPAPRPSLQHPRLLDH 359

QY 359 DHRSVEQVAVLASLGLSFLGLVAGALGLMLRLRRGKDGSPKPGFLASVIPPVDRRPP 418  
DB 359 DHRSVEQVAVLASLGLSFLGLVAGALGLMLRLRRGKDGSPKPGFLASVIPPVDRRPP 419

QY 419 GAPNL 423  
DB 420 GIPNL 424

RESULT 3  
JL0145  
Interleukin-6 receptor precursor (clone lambda 301) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 21-Jan-2000  
C:Accession: JL0145; S14543  
R:Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto,  
J. Exp. Med. 171, 2001-2009, 1990  
A:Title: Functional murine interleukin 6 receptor with the intracisternal a particle  
A:Reference number: JL0144; MUID:90278354  
A:Accession: JL0145  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-460 <SIG>  
A:Cross-references: GB:X51975; NID:G49725; PIDN:CAA36237.1; PID:G49726  
A:Experimental source: clone lambda 301  
R:Florillo, M.T.; Ciliberto, G.; Dente, L.  
submitted to the EMBL Data Library, July 1990  
A:Description: Cloning and expression of murine IL-6 receptor.  
A:Reference number: S14543  
A:Accession: S14543  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-373, 'R', 375-460 <PIO>  
A:Cross-references: EMBL:X53802; NID:G52692; PIDN:CAA37810.1; PID:G52693  
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu  
C:Keywords: cytokine receptor; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-460/Product: interleukin-6 receptor #status predicted <MAT>  
F:40-94/Domain: immunoglobulin homology <IMM>  
F:117-306/Domain: cytokine receptor homology <CRS>  
F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match 17.6%; Score 402; DB 2; Length 460;  
Best Local Similarity 30.6%; Pred. No. 2.4e-19;  
Matches 144; Conservative 55; Mismatches 184; Indels 88; Gaps 23;

QY 1 1MSSCSGLSRLVAVATALVSASSPCQAWGPPGYOGPGRSVKLCPCGVTAGDPVSWF 58  
DB 2 1TVGCTLLVALLAAAPVALVLS--CRALEVANGTIVSLPGATVTLICPGKEAGNVTH 59

QY 59 WFRDGEKLLQGD--SGLGHELVLAQADSTDEGTYICOTLDGALGGTTLQGLYPPARPV 117  
DB 60 WYISGS---QNRWTTTGTNTLVLDVQLSDTDGTYLC--SLNDHLVGTVPVLLVDVPEEPK 114

QY 118 VSC-QAADYENFSCWSPSQISGLPTRYLTSYRKKTIVLGADSQRRSPSPGWPCCP-QDPL 175  
DB 115 LSCFRKPNLVNAICEMRPSSTPS-PTTKAVLFAKKI-----NTTNGKSDFOVPCQYSQOL 168

QY 176 GAARCVVHGAFFWSQYRI-NYTEVNPGLGASTRLLDVSLQSLRPDPQGLRVSVPGYPR 234  
DB 169 KSFSCQVEILEGDKYHIVSLCVANSVGSKSHNEAFSLKMWQDPDPPANLVVSAIPGRP 228

QY 235 RGLRASWTYPASWPCQPHFLKFRLOYRPAQHAWSTVEPAGLVEVITDAVAGL 288

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 24, 2001, 17:33:26 ; Search time 24.52 Seconds  
(without alignments)  
1314.104 Million cell updates/sec

Title: US-09-532-263-5  
Perfect score: 2282  
Sequence: 1 MSSCSGLSRVLVAVATLV.....KPGFLASVIPVDRRPGAPNL 423

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2257.5	98.9	422	I37891	interleukin-11 rec
2	1879.5	82.4	432	I48343	interleukin-11 rec
3	402	17.6	460	JL0145	interleukin-6 rece
4	396	17.4	440	JL0144	interleukin-6 rece
5	374.5	16.4	372	I58141	ciliary neurotroph
6	368.5	16.1	362	S60614	growth promoting a
7	367.5	16.1	468	A41242	interleukin-6 rece
8	366.5	16.1	372	UHHUCN	ciliary neurotroph
9	306	13.4	462	A37986	interleukin-6 rece
10	222.5	9.8	830	I50455	prolactin receptor
11	216.5	9.5	831	JQ1655	prolactin receptor
12	207	9.1	581	I45971	prolactin receptor
13	195.5	8.6	616	A30304	prolactin receptor
14	191.5	8.4	310	A29884	prolactin receptor
15	191.5	8.4	412	A41070	prolactin receptor
16	191.5	8.4	610	A34631	lactogen receptor
17	191.5	8.4	610	A36116	prolactin receptor
18	189.5	8.3	622	A40144	prolactin receptor
19	183.5	8.0	1265	A37967	prolactin receptor
20	180	7.9	630	I51086	prolactin receptor
21	175.5	7.7	292	I77525	prolactin receptor
22	175.5	7.7	303	I77524	prolactin receptor
23	175.5	7.7	608	I53269	prolactin receptor
24	165	7.2	761	IJHUNG	prolactin receptor
25	160	7.0	328	A38957	neural cell adhesi
26	155.5	6.8	918	A36337	membrane glycopro
27	151.5	6.6	150	B34631	lactogen receptor
28	149.5	6.6	771	B38252	granulocyte colony
29	149.5	6.6	783	JH0329	granulocyte colony

## ALIGNMENTS

```
RESULT 1
I37891
interleukin-11 receptor alpha chain - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Dec-1999
C:Accession: I37891; G01970; G01971
R:Cherel, M.; Sorel, M.; Lebeau, B.; Dubois, S.; Moreau, J.F.; Bataille, R.; Minviell
Blood 86, 2534-2540, 1995
A:Title: Molecular cloning of two isoforms of a receptor for the human hematopoietic
A:Reference number: I37891; MUID:95399754
A:Accession: I37891
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-422 <RES>
A:Cross-references: EMBL:38102; NID:9955653; PIDN:CAA86224.1; PID:9955654
R:Van Leuven, F.
submitted to the EMBL Data Library, July 1995
A:Reference number: G08959
A:Accession: G01970
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-422 <VAN>
A:Cross-references: EMBL:U32323; NID:975334; PIDN:AAB36491.1; PID:975335
R:Van Leuven, F.
submitted to the EMBL Data Library, July 1995
A:Reference number: G08961
A:Accession: G01971
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-422 <VA2>
A:Cross-references: EMBL:U32324; NID:975336; PIDN:AAB36492.1; PID:975337
C:Genetics:
A:Introns: 34/1; 54/2; 111/1; 149/2; 160/2; 216/1; 270/3; 318/1; 358/1; 390/2; 418/1
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
F:120-310/Domain: cytokine receptor homology <CR>
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Query Match 98.9%; Score 2257.5; DB 2; Length 422;

Best Local Similarity 99.5%; Pred. No. 1.4e-141;

Matches 421; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MSSCSGLSRVLVAVATLVASSPCPQAWPGVQVGPGRSVKLCPCGVTAGDPVSWF 60

|||||

Db 1 MSSCSGLSRVLVAVATLVASSPCPQAWPGVQVGPGRSVKLCPCGVTAGDPVSWF 60

|||||

QY 61 RDGEPLKLGQPSGLGHELVLAQADSTDEGTTCQTLDGALGCTVTTLQGYPPARPVWSC 120

|||||

Db 61 RDGEPLKLGQPSGLGHELVLAQADSTDEGTTCQTLDGALGCTVTTLQGYPPARPVWSC 120

|||||

QY 121 QAADYENFSCWTNSPSQISGLPTRYLTYSRKKTVLGADSQRRSPSTGWPWCPQDPLGAARC 180

|||||

Db 121 QAADYENFSCWTNSPSQISGLPTRYLTYSRKKTVLGADSQRRSPSTGWPWCPQDPLGAARC 180

|||||

AAR50326  
ID AAR50326 standard; Protein; 265 AA.  
XX  
AC AAR50326;  
XX  
DT 19-OCT-1994 (first entry)  
XX  
DE Mouse soluble EPO receptor protein fragment.  
XX  
KW Murine; soluble; erythropoietin; EPO; receptor protein; SEPO-R; drug;  
KW antigen; diagnostic agent; biochemical reagent.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..25  
FT Protein /note= "Signal peptide"  
FT 26..265  
FT /note= "Mature EPO-R fragment"  
XX  
PN JP06038787-A.  
XX  
PD 15-FEB-1994.  
XX  
PF 04-MAR-1992; 92JP-0082865.  
XX  
PR 04-MAR-1992; 92JP-0082865.  
XX  
PA (SNOW ) SNOW BRAND MILK PROD CO LTD.  
XX  
DR WPI; 1994-094847/12.  
DR N-PSDB; AAQ44853.  
XX  
PT Soluble erythropoietin receptor protein - and DNA coding for  
PT SEPO-R, useful as diagnostic reagent  
XX  
PS Disclosure; Page 5-6; 9pp; Japanese.  
XX  
CC This sequence represents a fragment of the murine soluble erythro-  
CC poietin (EPO) receptor protein (SEPO-R). This protein is able to  
CC bind to EPO and has antigenicity as an EPO receptor. The molecular  
CC weight of the full length protein is pref 33 or 29 kD. The protein  
CC is useful as a drug, as a diagnostic agent and a biochemical reagent.  
XX  
SQ Sequence 265 AA;

Query Match 96.8%; Score 30; DB 15; Length 265;  
Best Local Similarity 80.0%; Pred. NO. 5.5e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5  
Db 232 wsaws 236

Search completed: August 24, 2001, 17:32:30  
Job time: 113 sec

QY 1 WSXWS 5  
DB 200 wsaws 204

## RESULT 13

AAB40915  
ID AAB40915 standard; Protein; 221 AA.

AC AAB40915;

DT 08-FEB-2001 (first entry)

XX Human ORFX ORF679 polypeptide sequence SEQ ID NO:1358.

XX Human; open reading frame; ORFX: detection; cytotstatic; hepatotropic;  
KW vulnary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;  
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;  
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
KW cholesterol ester storage; systemic lupus erythematosus; infection;  
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
KW thrombosis; contraceptive.

XX Homo sapiens.

OS  
XX WO200058473-A2.

PN  
XX 05-OCT-2000.

PD  
XX 31-MAR-2000; 2000WO-US08621.

XX 31-MAR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127636.

PR 05-APR-1999; 99US-0127728.

PR 30-MAR-2000; 2000US-0540763.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI: 2000-602362/57.

DR N-PSDB; AAC75124.

XX Novel nucleic acids and peptides derived from open reading frame X,  
PT useful for treating e.g. cancers, proliferative disorders,  
PT neurodegenerative disorders and cardiovascular disease -

XX Claim 11; Page 1158-1159; 5507pp; English.

XX AACT74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
CC sequences have activities such as: cytotstatic; hepatotropic; vulnary;  
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;  
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;  
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;  
CC antidiabetic; hypotensive; dermatological; immunosuppressive;  
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;  
CC antithyroid; and antianaemic. The sequences can be used for determining  
CC the presence of or predisposition to, or preventing or treating  
CC pathological conditions associated with an ORFX-associated disorder. The  
CC nucleic acids can be used to express ORFX proteins in gene therapy  
CC vectors. The proteins and nucleic acids may be used to treat cancers,  
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,

CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance  
CC coagulation; to inhibit thrombosis; and as a contraceptive.

SQ Sequence 221 AA;

Query Match 96.8%; Score 30; DB 21; Length 221;

Best Local Similarity 80.0%; Pred. No. 4.7e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5

DB 23 wsaws 27

## RESULT 14

AAB21685

ID AAB21685 standard; peptide; 225 AA.

XX AAB21685;

XX AAB21685;

DT 21-DEC-2000 (first entry)

XX Human mature erythropoietin receptor EPOR extracellular domain #1.

DE Human mature erythropoietin receptor EPOR extracellular domain #1.

XX Ligand; cell surface receptor; erythropoietin; EPOR; human.

XX Homo sapiens.

XX WO200047612-A2.

PN  
XX 17-AUG-2000.

PD  
XX 11-FEB-2000; 2000WO-US03665.

XX 11-FEB-1999; 99US-0120009.

PR 29-APR-1999; 99US-0131674.

XX (XENC-) XENCOR INC.

XX Luo P, Dahiyat B;

XX WPI: 2000-549135/50.

XX Screening for ligand analogs and agents which modulate ligand-receptor  
PT binding, comprises adding a test ligand to a non-naturally occurring  
PT cell surface receptor analog -

XX Example 1; Fig 8; 82pp; English.

XX The present invention relates to a method for screening for a ligand  
CC analog, comprising adding a candidate ligand to a non-naturally occurring  
CC cell surface receptor analog e.g. erythropoietin receptor (EPOR), and  
CC determining the binding of the ligand to the analog. The present sequence  
CC is a mature human erythropoietin receptor (EPOR) extracellular domain.  
CC This sequence may be used in the present invention as a cell surface  
CC receptor analog.

XX Sequence 225 AA;

Query Match 96.8%; Score 30; DB 21; Length 225;

Best Local Similarity 80.0%; Pred. No. 4.7e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5

DB 209 wsaws 213

## RESULT 15

XX (GETH ) GENENTECH INC.  
 XX Bass SH, Cunningham BC, Fuh G, Lowman HB, Matthews DJ;  
 PI Wells JA;  
 XX WPI; 1992-096838/12.  
 XX New method of modifying polypeptide hormone-receptor complex - to  
 PT produce human growth hormone variant, useful for stimulating  
 PT lactogenic and somatogenic response  
 XX  
 PS Disclosure; Page 41; 74pp; English.  
 XX This truncated human prolactin binding protein is encoded by the  
 CC insert contained in plasmid pPRLbp(1-211). The hPRLbp gene fragment  
 CC is transcribed under the control of the alkaline phosphatase  
 CC promoter and secreted into the host (E.coli) periplasm under the  
 CC direction of the stII signal sequence. A stop codon and MluI  
 CC restriction site were introduced after the threonine 211 codon which  
 CC immediately precedes the transmembrane domain of the receptor. The  
 CC plasmid was used as a template for site-directed mutagenesis to  
 CC modify the metal-chelating centre of the protein. See, e.g. AAR24273  
 CC for an example of a preferred variant.  
 XX  
 SQ Sequence 211 AA;

Query Match 96.8%; Score 30; DB 13; Length 211;  
 Best Local Similarity 80.0%; Pred. NO. 4.4e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WSXWS 5  
 || ||  
 Db 191 wsaws 195

RESULT 11  
 AAR24273  
 ID AAR24273 standard; Protein; 211 AA.  
 XX  
 AC AAR24273;  
 XX  
 DT 20-JUL-1992 (first entry)  
 XX  
 DE Truncated human prolactin binding protein variant.  
 XX  
 KW hPRLbp; placental lactogen; zinc finger; chelate;  
 KW receptor-ligand complex.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 188  
 FT /note= "wild-type His replaced by Ala"  
 XX  
 PN WO9203478-A.  
 XX  
 PD 05-MAR-1992.  
 XX  
 PF 16-AUG-1991; 91WO-US05856.  
 XX  
 PR 17-AUG-1990; 90US-0568936.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Bass SH, Cunningham BC, Fuh G, Lowman HB, Matthews DJ;  
 PI Wells JA;  
 XX  
 DR WPI; 1992-096838/12.  
 XX  
 PT New method of modifying polypeptide hormone-receptor complex - to  
 PT produce human growth hormone variant, useful for stimulating

PT lactogenic and somatogenic response  
 XX  
 PS Claim 41; Page 56; 74pp; English.  
 XX  
 CC Plasmid pPRLbp(1-211) (see AAR22228) coding for truncated, soluble  
 CC prolactin binding protein was mutagenised such that the His codon  
 CC at position 188 was substituted by an Ala codon. The hPRLbp variant  
 CC has altered binding affinity for hGH.  
 XX  
 SQ Sequence 211 AA;

Query Match 96.8%; Score 30; DB 13; Length 211;  
 Best Local Similarity 80.0%; Pred. NO. 4.4e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WSXWS 5  
 || ||  
 Db 191 wsaws 195

RESULT 12  
 AAB21686  
 ID AAB21686 standard; peptide; 211 AA.  
 XX  
 AC AAB21686;  
 XX  
 DT 21-DEC-2000 (first entry)  
 XX  
 DE Human mature erythropoietin receptor EPOR, extracellular domain #2.  
 XX  
 KW Ligand; cell surface receptor; erythropoietin; EPOR; human;  
 KW protein design automation; PDA.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200047612-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 11-FEB-2000; 2000WO-US03665.  
 XX  
 PR 11-FEB-1999; 99US-0120009.  
 PR 29-APR-1999; 99US-0131674.  
 XX  
 PA (XENC-) XENCOR INC.  
 XX  
 PI Luo P, Dahiyat B;  
 XX  
 DR WPI; 2000-549135/50.  
 XX  
 PT Screening for ligand analogs and agents which modulate ligand-receptor  
 PT binding, comprises adding a test ligand to a non-naturally occurring  
 PT cell surface receptor analog -  
 XX  
 PS Example 1; Fig 8; 82pp; English.  
 XX  
 CC The present invention relates to a method for screening for a ligand  
 CC analog, comprising adding a candidate ligand to a non-naturally occurring  
 CC cell surface receptor analog e.g. erythropoietin receptor (EPOR), and  
 CC determining the binding of the ligand to the analog. The present sequence  
 CC is a mature human erythropoietin receptor (EPOR) extracellular domain.  
 CC Protein Design Automation was carried out on the present sequence, so  
 CC that it may be used in the present invention as a cell surface receptor  
 CC analog.  
 XX  
 SQ Sequence 211 AA;

Query Match 96.8%; Score 30; DB 21; Length 211;  
 Best Local Similarity 80.0%; Pred. NO. 4.4e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

PN WO200119860-A2.  
 XX 22-MAR-2001.  
 PD  
 PF 14-SEP-2000; 2000WO-US25435.  
 XX  
 PR 15-SEP-1999; 99US-0154140.  
 PR 06-DEC-1999; 99US-0169155.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 XX Tang YT, Hillman JL, Yue H, Reddy R, Lal P, Shah P, Azimzai Y;  
 PI Baughn MR, Lu DAM, Bandman O, Shih LL, Patterson C;  
 XX  
 DR WPI; 2001-211447/21.  
 DR N-PSDB; AAC85557.  
 XX  
 XX Isolated polypeptides and polynucleotides involved in cell  
 PT differentiation are used for treatment, prevention and diagnosis of  
 PT cell proliferative, developmental and neurological disorders e.g.  
 PT cancer and Alzheimer's disease -  
 XX  
 XX Claim 1; Page 109; 137pp; English.  
 XX  
 CC The sequences given in AB47123-50 show human polypeptides involved  
 CC in cell differentiation (CDIFF). CDIFF polypeptides and agonists of  
 CC these are used to treat a disease or condition associated with  
 CC decreased expression of functional CDIFF. An antagonist of CDIFF is  
 CC used to treat a disease or condition associated with over expression  
 CC of functional CDIFF. CDIFF polypeptides may be used for the treatment,  
 CC prevention and diagnosis of cell proliferative, developmental and  
 CC neurological disorders, such as Alzheimer's disease, schizophrenia  
 CC disorders, arteriosclerosis, cancer, atherosclerosis, diabetes mellitus  
 CC and epilepsy. The CDIFF-16 sequence is homologous to Bos. taurus  
 CC beta-A2 crystallin.  
 XX  
 XX Sequence 197 AA;  
 SQ

Query Match 96.8%; Score 30; DB 22; Length 197;  
 Best Local Similarity 80.0%; Pred. No. 4.2e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5  
 || ||  
 Db 78 wsaws 82

RESULT 9  
 AAB08135  
 ID AAB08135 standard; Protein; 206 AA.  
 AC AAB08135;  
 XX  
 XX 04-DEC-2000 (first entry)  
 DT  
 XX  
 XX Amino acid sequence of a KIAA0550 polypeptide.  
 XX  
 XX Type 1 repeat; thrombospondin-1; TSP-1; Type 1 repeat peptide; TRP;  
 KW KIAA0688; KIAA0550; angiogenesis inhibitory protein; angiogenesis;  
 KW cancer; tumour; rheumatoid arthritis; psoriasis; retinopathy;  
 KW ocular angiogenic disease; macular degeneration; corneal graft rejection;  
 KW neovascular glaucoma; retrolental fibroplasia; rubeosis;  
 KW Osler-Webber Syndrome; myocardial angiogenesis; haemophilic joint;  
 KW plaque neovascularisation; telangiectasia; angiofibroma;  
 KW wound granulation; coronary collateral; cerebral collateral;  
 KW arteriovenous malformation; ischemic limb angiogenesis;  
 KW neovascular glaucoma; retrolental fibroplasia; fracture; vasculogenesis;  
 KW heliobacter related disease; hematopoiesis; ovulation; menstruation;  
 KW placental; birth control; embryo implantation.  
 XX  
 XX Homo sapiens.  
 OS

PN WO200047622-A2.  
 XX 17-AUG-2000.  
 PD  
 PF 15-FEB-2000; 2000WO-GB00520.  
 XX  
 PR 15-FEB-1999; 99GB-0003408.  
 XX  
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
 XX  
 XX Mazarakis N, Martin-Rendon E, Kingsman SM;  
 PI WPI; 2000-549137/50.  
 DR  
 XX  
 XX Non-naturally occurring Type I repeat peptide (TRP) derived from human  
 PT thrombospondin-1, KIAA0688 or KIAA0550 proteins, useful in the  
 PT treatment of angiogenesis and/or cancer -  
 XX  
 XX Claim 5; Fig 7; 84pp; English.  
 PS  
 XX The present sequence represents a KIAA0550 polypeptide. The  
 CC specification describes a non-naturally occurring Type I repeat peptide  
 CC (TRP), derived from human thrombospondin-1 (HTSP-1), KIAA0688 or KIAA0550  
 CC proteins. The TRP protein is an angiogenesis inhibitory protein. TRP  
 CC proteins are used for the treatment of conditions associated with  
 CC angiogenesis and cancer. Angiogenic mediated-diseases include tumours,  
 CC rheumatoid arthritis, psoriasis, ocular angiogenic diseases, retinopathy  
 CC of prematurity, macular degeneration, corneal graft rejection,  
 CC neovascular glaucoma, retrolental fibroplasia, rubeosis), Osler-Webber,  
 CC Syndrome, myocardial angiogenesis, plaque neovascularisation,  
 CC telangiectasia, haemophilic joints, angiofibroma, wound granulation,  
 CC coronary collaterals, cerebral collaterals, arteriovenous malformations,  
 CC ischemic limb angiogenesis, neovascular glaucoma, retrolental  
 CC fibroplasia, heliobacter related diseases, fractures, vasculogenesis,  
 CC hematopoiesis, ovulation, menstruation and placental. TRPs are also  
 CC useful in the treatment of disease of excessive or abnormal stimulation  
 CC of endothelial cells. TRP can also be used as a birth control agent, as  
 CC it prevents the vascularisation required for embryo implantation.  
 XX  
 XX Sequence 206 AA;  
 SQ

Query Match 96.8%; Score 30; DB 21; Length 206;  
 Best Local Similarity 80.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5  
 || ||  
 Db 108 wsaws 112

RESULT 10  
 AAR22228  
 ID AAR22228 standard; protein; 211 AA.  
 AC AAR22228;  
 XX  
 XX 20-JUL-1992 (first entry)  
 DT  
 XX  
 XX Truncated human prolactin binding protein.  
 DE  
 XX hPRLbp; placental lactogen; zinc finger; chelate;  
 KW receptor-ligand complex.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO9203478-A.  
 PN  
 XX 05-MAR-1992.  
 PD  
 XX 16-AUG-1991; 91WO-US05856.  
 PF  
 XX 17-AUG-1990; 90US-0568936.  
 PR



DT 05-NOV-1992 (first entry)  
 XX Partial MPLV-env related polypeptide.  
 XX  
 DE  
 XX  
 KW Myeloproliferative leukaemia virus; envelope protein; gp70;  
 KW haematopoietic cell; Growth Factor receptor.  
 XX  
 OS Myeloproliferative leukaemia virus.  
 XX  
 PN W09207074-A.  
 XX  
 PD 30-APR-1992.  
 XX  
 PF 19-OCT-1990; 90WO-FR00762.  
 XX  
 PR 19-OCT-1990; 90WO-FR07623.  
 XX  
 PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX  
 PI Charon M, Gisselbrecht S, Penciolelli JF, Souyri M;  
 PI Tambourin P, Varlet P, Vigon I, Wendling F;  
 XX  
 DR WPI; 1992-167154/20.  
 DR N-PSDB; AAQ24676.  
 XX  
 XX Polypeptides similar to v-mlp protein of MPLV - for diagnosis and  
 PT treatment of myeloproliferative diseases  
 PT  
 XX  
 PS Claim 4; Page 31; 75pp; French.  
 XX  
 CC This polypeptide is an example of a fragment related to the MPLV  
 CC env protein having the amino acid sequence assigned GENESEQ  
 CC accession number AAR23970. The protein is involved in the  
 CC ligand-fixing or signal-transmitting function of haematopoietic  
 CC growth factor receptors; is recognised by antibodies to the  
 CC protein AAR23970; when produced from the MPLV genome it can induce/  
 CC promote proliferation of haematopoietic cells and/or is involved  
 CC in differentiation of haematopoietic cells.  
 CC See also AAQ24674-7.  
 XX  
 XX Sequence 184 AA;  
 SQ

Query Match 96.8%; Score 30; DB 13; Length 184;  
 Best Local Similarity 80.0%; Pred. No. 3.9e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5  
 || ||  
 Db 26 wsws 30

RESULT 7  
 AAY18046  
 ID AAY18046 standard; Protein; 190 AA.  
 XX  
 AC AAY18046;  
 XX  
 DT 03-AUG-1999 (first entry)  
 XX  
 DE Human mpl mutant protein sequence.  
 XX  
 KW Human; mpl; mutein; cytokine receptor; secretory signal; detection;  
 KW extracellular region; membrane protein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN W09926978-A1.  
 XX  
 PD 03-JUN-1999.  
 XX  
 PF 26-NOV-1998; 98WO-JP05326.

XX 26-NOV-1997; 97JP-0324912.  
 PR  
 XX (CHUS ) CHUGAI SEIYAKU KK.  
 PA (KITA/) KITAMURA T.  
 XX  
 PI Kitamura T, Kojima T;  
 XX  
 DR WPI; 1999-347694/29.  
 DR N-PSDB; AAX76826.  
 XX  
 PT DNA encoding human mpl fragment lacking secretory signal, is  
 PT incorporated into a vector for detection of secretory proteins by  
 PT induction of homeopoietic cell proliferation  
 XX  
 PS Claim 5; Page 24-26; 47pp; Japanese.  
 XX  
 CC This sequence is a human mpl mutant protein.  
 CC The invention relates to a peptide derived from a cytokine receptor such  
 CC as human mpl but lacking the secretory signal and most of the  
 CC extracellular region. The invention also relates to a method for  
 CC isolating cDNA encoding a secretory protein. The method is used for  
 CC detection of secretory proteins (including type 1 and type 2 membrane  
 CC proteins) in cDNA libraries.  
 XX  
 SQ Sequence 190 AA;

Query Match 96.8%; Score 30; DB 20; Length 190;  
 Best Local Similarity 80.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5  
 || ||  
 Db 29 wsws 33

RESULT 8  
 AAB47135  
 ID AAB47135 standard; Protein; 197 AA.  
 XX  
 AC AAB47135;  
 XX  
 DT 04-JUN-2001 (first entry)  
 XX  
 DE CDIFF-16, Incyte ID No. 3495166CD1.  
 XX  
 KW Human; cell differentiation; CDIFF; agonist; antagonist; epilepsy;  
 KW cell proliferation; Alzheimer's disease; schizophrenic disorder;  
 KW arteriosclerosis; cancer; atherosclerosis; diabetes mellitus.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 15  
 FT /note= "Potential phosphorylation site"  
 FT Modified-site 47  
 FT /note= "Potential phosphorylation site"  
 FT Modified-site 94  
 FT /note= "Potential phosphorylation site"  
 FT Modified-site 104  
 FT /note= "Potential glycosylation site"  
 FT Modified-site 109  
 FT /note= "Potential phosphorylation site"  
 FT Modified-site 142  
 FT /note= "Potential phosphorylation site"  
 FT Modified-site 176  
 FT /note= "Potential phosphorylation site"  
 FT Modified-site 177  
 FT /note= "Potential phosphorylation site"  
 FT Modified-site 191  
 FT /note= "Potential phosphorylation site"  
 XX

QY 1 WSXWS 5  
DB 38 WSWWS 42

## RESULT 4

AAB51501  
ID AAB51501 standard; Protein; 48 AA.

XX AC

DT 16-FEB-2001 (first entry)

DE Human secreted protein BLAST search protein SEQ ID NO: 178.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;  
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; human; secreted protein.

XX OS Homo sapiens.

XX WO200058495-A1.

XX 05-OCT-2000.

XX 23-MAR-2000; 2000WO-US07661.

XX 26-MAR-1999; 99US-0126504.

XX 07-JAN-2000; 2000US-0174847.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM, Komatsoulis G;

XX WPI; 2000-611720/58.

XX New nucleic acid molecules encoding 45 human secreted proteins for  
PT diagnosing, preventing, treating or ameliorating medical conditions and  
PT used as food additives or preservatives.

PS Disclosure; Page 404; 410pp; English.

XX The invention relates to the isolation of genes AAC93310-C93354 encoding  
CC the human secreted proteins AAB51380-B51423. The genes and proteins are  
CC useful for preventing, ameliorating or treating medical conditions, e.g.  
CC by protein or gene therapy. The genes are isolated from a range of human  
CC tissues disclosed in the specification. The nucleic acids, proteins,  
CC antibodies and (ant)agonists are useful in the diagnosis, treatment and  
CC prevention of: (a) cancer, e.g. breast and ovarian cancer, and other  
CC cancers of the adrenal gland, bone, bone marrow, breast,  
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders  
CC e.g. Addison's disease, allergies, autoimmune haemolytic anaemia,  
CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple  
CC sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
CC cardiovascular disorders such as myocardial ischaemias; (d) wound  
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;  
CC and (f) infectious diseases such as viral, bacterial, fungal and  
CC parasitic infections. The present sequence is a protein isolated in the  
CC present invention.

XX Sequence 48 AA;

Query Match 96.8%; Score 30; DB 21; Length 48;  
Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5  
DB 38 WSWWS 42

## RESULT 5

AAY76592  
ID AAY76592 standard; Protein; 82 AA.

XX AC AAY76592;

DT 10-APR-2000 (first entry)

DE Human ovarian tumor EST fragment encoded protein 88.

XX Expressed sequence tag; EST; human; ovarian tumor; anticancer;  
KW gene therapy; treatment.

XX OS Homo sapiens.

XX DE19817557-A1.

XX 21-OCT-1999.

XX 09-APR-1998; 98DE-1017557.

XX 09-APR-1998; 98DE-1017557.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

XX WPI; 1999-591920/51.

XX N-PSDB; AAZ77487.

XX New nucleic acid sequences expressed in ovarian, and some other, cancer  
PT tissues, and derived polypeptides, for treatment of ovarian cancer and  
PT identification of therapeutic agents.

PS Claim 25; Page 279; 310pp; German.

XX This invention describes novel nucleic acid (cDNA) sequences (A) which  
CC have anticancer activity and are highly expressed in ovarian tumor  
CC tissue (and some also in testis and breast cancer tissue). The products  
CC of the invention can be used for gene therapy. (A) are used (i) for  
CC recombinant expression of polypeptides (B) and (ii) to isolate complete  
CC ovarian cancer; (ii) directly for treating this form of cancer  
CC (including expression from gene therapy vectors) and (iii) for generation  
CC of specific antibodies. (A) are identified by assembling ESTs (expressed  
CC sequence tags) from a particular tissue type before comparison of  
CC expression patterns. This allows a significantly longer fragment of the  
CC gene to be revealed, so should reduce the number of failures associated  
CC with the fact that ESTs from different libraries may represent different  
CC parts of the same unknown gene, distorting the estimated frequency of  
CC occurrence in a particular tissue. AAY76505-Y76638 represent protein  
CC fragments encoded by the human ovarian tumor cDNA library derived EST  
CC fragments represented in AAZ77450-Z77572.

XX Sequence 82 AA;

Query Match 96.8%; Score 30; DB 20; Length 82;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5

DB 8 WSWWS 12

## RESULT 6

AAR27660  
ID AAR27660 standard; Protein; 184 AA.

XX AC AAR27660;

XX

PS Claim 8; Page 63; 67pp; English.

XX The peptides AAR69780-90 are active peptide fragments based on the  
CC second type 1 repeat sequence (amino acids 412-473) of thrombospondin  
CC (sequence not given in the specification) which can be used to inhibit  
CC the stimulation of transforming growth factor-beta (TGF- $\beta$ ) from latent  
CC TGF- $\beta$ . The inhibitory peptides can be used to prevent fibrosis or block  
CC TGF- $\beta$  mediated endothelial cell proliferation. Peptides (see  
CC AAR69766-79) which stimulate the conversion of latent TGF- $\beta$  to active  
CC TGF- $\beta$  can be used to enhance wound healing.

XX Sequence 5 AA;

Query Match 96.8%; Score 30; DB 16; Length 5;

Best Local Similarity 80.0%; Pred. No. 3.4e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5

DB 1 WSSWS 5

RESULT 2

AAR98939

ID AAR98939 standard; peptide; 32 AA.

AC AAR98939;

DT 28-SEP-1996 (first entry)

DE Synthetic human erythropoietin receptor peptide, SE-9.

XX Monoclonal antibody; erythropoietin receptor; diagnosis; anaemia;  
KW erythropoiesis; erythrocyte production; epitope mapping.

XX Synthetic.

XX WO9603438-A1.

XX 08-FEB-1996.

XX 26-JUL-1995; 95WO-US09458.

XX 26-JUL-1994; 94US-0280864.

XX (AMGE-) AMGEN INC.

XX Elliott SG;

XX WPI; 1996-117004/12.

XX Monoclonal antibodies stimulating an erythropoietin receptor -  
PT useful in diagnosis and treatment of patients having disorders  
PT associated with low red blood cell levels, e.g. anaemia

XX Example 6; Page 34; 61pp; English.

XX AAR9960-R9965 and AAR98936-R98939 are overlapping, synthetic human  
CC erythropoietin receptor (shuEPOR) peptides which span residues 1 to  
CC 244 of the human EPOR. The peptides are used to map the EPOR binding  
CC epitope of an EPOR monoclonal antibody which binds to EPORs and  
CC stimulates erythropoiesis by stimulating the proliferation and/or  
CC differentiation of erythroid progenitor cells to erythrocytes.  
CC Pharmaceutical compns. contg. the antibody may be used in the  
CC diagnosis and treatment of patients having disorders associated with  
CC low red blood cell levels, e.g. anaemia. The antibodies are also  
CC useful in methods and kits for detecting EPORs in biological in  
CC biological samples.

XX Sequence 32 AA;

Query Match 96.8%; Score 30; DB 21; Length 48;

Best Local Similarity 80.0%; Pred. No. 1.1e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 96.8%; Score 30; DB 17; Length 32;

Best Local Similarity 80.0%; Pred. No. 72;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5

DB 16 WSAWS 20

RESULT 3

AAB51497

ID AAB51497 standard; Protein; 48 AA.

XX AAB51497;

DT 16-FEB-2001 (first entry)

XX Human secreted protein BLAST search protein SEQ ID NO: 174.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
KW anti-allergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;  
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; human; secreted protein.

XX Homo sapiens.

XX WO200058495-A1.

XX 05-OCT-2000.

XX 23-MAR-2000; 2000WO-US07661.

XX 26-MAR-1999; 95US-0126504.

XX 07-JAN-2000; 2000US-0174847.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

XX WPI; 2000-611720/58.

XX New nucleic acid molecules encoding 45 human secreted proteins for  
PT diagnosing, preventing, treating or ameliorating medical conditions and  
PT used as food additives or preservatives -

XX Disclosure; Page 402; 410pp; English.

XX The invention relates to the isolation of genes AAC93310-C93354 encoding  
CC the human secreted proteins AAB51380-B51423. The genes and proteins are  
CC useful for preventing, ameliorating or treating medical conditions, e.g.  
CC by protein or gene therapy. The genes are isolated from a range of human  
CC tissues disclosed in the specification. The nucleic acids, proteins,  
CC antibodies and (antagonists are useful in the diagnosis, treatment and  
CC prevention of: (a) cancer, e.g. breast and ovarian cancer, and other  
CC cancers of the adrenal gland, bone, bone marrow, breast,  
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders  
CC e.g. Addison's disease, allergies, autoimmune haemolytic anaemia,  
CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple  
CC sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
CC cardiovascular disorders such as myocardial ischaemia; (d) wound  
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;  
CC and (f) infectious diseases such as viral, bacterial, fungal and  
CC parasitic infections. The present sequence is a protein isolated in the  
CC present invention.

XX Sequence 48 AA;

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: August 24, 2001, 17:30:37 ; Search time 32.57 Seconds  
(without alignments)  
9.307 Million cell updates/sec

Title: US-09-532-263-1

Perfect score: 31

Sequence: 1 WSXWS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_0601.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
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15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	ID	Description
1	30	96.8	5 16 AAR69782	Thrombospondin-der
2	30	96.8	32 17 AAR98939	Synthetic human er
3	30	96.8	48 21 AAB51497	Human secreted pro
4	30	96.8	48 21 AAB51501	Human secreted pro
5	30	96.8	82 20 AAY76592	Human ovarian tumo
6	30	96.8	184 13 AAR27660	Partial MPLV-env r
7	30	96.8	190 20 AAY18046	Human mpl mutant p
8	30	96.8	197 22 AAB47135	CDIFF-16, Incyte I
9	30	96.8	206 21 AAB08135	Amino acid sequenc
10	30	96.8	211 13 AAR22228	Truncated human pr
11	30	96.8	211 13 AAR24273	Truncated human pr

12	30	96.8	211	21 AAB21686	Human mature eryth
13	30	96.8	221	21 AAB40915	Human ORFX ORF679
14	30	96.8	225	21 AAB21685	Human mature eryth
15	30	96.8	265	15 AAR50326	Mouse soluble EPO
16	30	96.8	284	13 AAR23971	MPLV env-vmpl fusi
17	30	96.8	334	20 AAY18047	Human mpl-GM-CSF f
18	30	96.8	334	20 AAY18048	Human mpl-GM-CSF f
19	30	96.8	349	21 AAY96921	Soluble human prol
20	30	96.8	349	21 AAY95527	Human prolactin re
21	30	96.8	370	22 AAB50684	C. elegans UNC-5 p
22	30	96.8	379	21 AAY59390	Murine soluble int
23	30	96.8	380	21 AAG08922	Arabidopsis thalia
24	30	96.8	380	21 AAG54208	Arabidopsis thalia
25	30	96.8	382	13 AAR27659	MPLV-env related p
26	30	96.8	385	21 AAG27840	Arabidopsis thalia
27	30	96.8	397	21 AAG08921	Arabidopsis thalia
28	30	96.8	397	21 AAG54207	Arabidopsis thalia
29	30	96.8	400	12 AAR10919	Human GM-CSF recep
30	30	96.8	415	21 AAB58729	Breast and ovarian
31	30	96.8	422	17 AAR9090	Human interleukin-
32	30	96.8	422	22 AAB36654	Human IL-11 recept
33	30	96.8	423	17 AAR92814	Human interleukin-
34	30	96.8	432	17 AAR92813	Murine interleukin
35	30	96.8	432	22 AAB36653	Mouse IL-11 recept
36	30	96.8	438	21 AAY44622	Truncated human Ep
37	30	96.8	438	21 AAY44623	R154C truncated hu
38	30	96.8	441	17 AAR9091	Murine Etl-2 gene
39	30	96.8	482	16 AAR75941	Soluble murine MPL
40	30	96.8	488	18 AAW08349	EpoRfc fusion prot
41	30	96.8	503	21 AAB13012	Q-tagged erythrope
42	30	96.8	507	11 AAR06511	EPO receptor seque
43	30	96.8	507	15 AAR47517	MEL EPO receptor.
44	30	96.8	507	15 AAR50327	Mouse soluble EPO
45	30	96.8	507	16 AAR69502	Mouse erythropoiet

## ALIGNMENTS

RESULT 1

AAR69782

ID AAR69782 standard; peptide; 5 AA.

AC AAR69782;

XX 13-OCT-1995 (first entry)

DT 13-OCT-1995 (first entry)

XX Thrombospondin-derived TGF-beta inhibitory peptide #2.

XX Thrombospondin type 1 repeat sequence; transforming growth factor-beta;  
KW wound healing; fibrosis; endothelial cell proliferation.  
XX Synthetic.

XX WO9505191-A.

XX 23-FEB-1995.

XX 12-AUG-1994; 94WO-US09193.

XX 13-AUG-1993; 93US-0106120.

XX 04-MAY-1994; 94US-0238169.

XX (UABR-) UAB RES FOUND.

XX Krutzsch HC, Murphy-Ullrich JE, Roberts DD, Schultz-Cherry S;

XX WPI; 1995-098579/13.

XX Stimulating or inhibiting transforming growth factor-beta by

XX contacting with thrombo-spondin or an activating enzyme - used

XX to enhance wound healing or prevent fibrosis

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CC -!- FUNCTION: A POSITIVE REGULATOR OF THE ALTERNATE PATHWAY OF  
CC COMPLEMENT. IT BINDS TO AND STABILIZES THE C3-AND C5-CONVERTASE  
CC ENZYME COMPLEXES.  
CC -!- SIMILARITY: CONTAINS 6 TSP TYPE-1 DOMAINS.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X12905; CAA31389.1; -  
CC DR PIR; S05478; S05478.  
CC DR MGD; MGI:97545; Pfc.  
CC DR InterPro: IPR000884; -  
CC DR Pfam; PF00090; TSP\_1; 6.  
CC DR PROSITE; PS50092; TSP1; 6.  
CC KW Complement alternate pathway; Glycoprotein; Repeat.  
CC FT NON\_TER 1  
CC FT DOMAIN 46 103 TSP TYPE-1 1.  
CC FT DOMAIN 104 160 TSP TYPE-1 2.  
CC FT DOMAIN 161 224 TSP TYPE-1 3.  
CC FT DOMAIN 225 282 TSP TYPE-1 4.  
CC FT DOMAIN 283 345 TSP TYPE-1 5.  
CC FT DOMAIN 346 405 TSP TYPE-1 6.  
CC FT CARBOHYD 396 396 N-LINKED (GLCNAC... ) (POTENTIAL).  
CC SQ SEQUENCE 437 AA; 47538 MW; 2B8DBCE22B3B78BE CRC64;

Query Match 96.8%; Score 30; DB 1; Length 437;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 WSXWS 5  
DB 49 WSAWS 53

RESULT 15  
ADRO\_MOUSE  
ID ADRO\_MOUSE STANDARD; PRT; 494 AA.  
AC Q61578;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE NADPH:ADRENODOXIN OXIDOREDUCTASE, MITOCHONDRIAL PRECURSOR  
DE (EC 1.18.1.2) (ADRENODOXIN REDUCTASE) (AR) (FERREDOXIN-NADP(+)  
DE REDUCTASE).  
GN FDXR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Kidney;  
RX MEDLINE=96085117; PubMed=7495857;  
RA Itoh S., Iemura O., Yamada E., Yoshimura T., Tsujikawa K., Kohama Y.,  
RA Mimura T.;  
RT "cDNA cloning of mouse ferredoxin reductase from kidney.";  
RL Biochim. Biophys. Acta 1264:159-162(1995).  
CC -!- FUNCTION: SERVES AS THE FIRST ELECTRON TRANSFER PROTEIN IN ALL THE  
CC MITOCHONDRIAL P450 SYSTEMS. INCLUDING CHOLESTEROL SIDE CHAIN  
CC CLEAVAGE IN ALL STEROIDGENIC TISSUES, STEROID 11-BETA  
CC HYDROXYLATION IN THE ADRENAL CORTEX, 25-OH-VITAMIN D3-24  
CC HYDROXYLATION IN THE KIDNEY, AND STEROL C-27 HYDROXYLATION IN THE  
CC LIVER.  
CC -!- CATALYTIC ACTIVITY: REDUCED ADRENODOXIN + NADP(+) = OXIDIZED  
CC ADRENODOXIN + NADPH.  
CC -!- COFACTOR: FAD.  
CC -!- PATHWAY: CHOLESTEROL SIDE-CHAIN-CLEAVAGE SYSTEM.

CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE ADRENAL, TESTIS AND OVARY AND  
CC TO A LESSER EXTENT IN THE LIVER AND KIDNEY.  
CC  
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CC  
CC EMBL; D49920; BAA08659.1; -  
CC DR MGD; MGI:104724; Fdxr.  
CC DR InterPro: IPR000759; -  
CC DR PRINTS; PR00419; ADXEDTASE.  
CC KW Electron transport; Oxidoreductase; Flavoprotein; NADP; FAD;  
CC Mitochondrion; Transit peptide.  
CC FT TRANSIT 1 34  
CC FT CHAIN 35 494 NADPH:ADRENODOXIN OXIDOREDUCTASE.  
CC SQ SEQUENCE 494 AA; 54202 MW; 4BD279DFC606A5C5 CRC64;  
Query Match 96.8%; Score 30; DB 1; Length 494;  
Best Local Similarity 80.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 WSXWS 5  
DB 11 WSAWS 15

Search completed: August 24, 2001, 17:34:32  
Job time: 160 sec





Proc. Natl. Acad. Sci. U.S.A. 82:4356-4359(1985).

-!- SUBCELLULAR LOCATION: SECRETED.

-!- DEVELOPMENTAL STAGE: PLACENTAL LACTOGEN I IS EXPRESSED IN MID-PREGNANCY, WHILE PLACENTAL LACTOGEN II IS EXPRESSED THROUGHOUT THE LATER HALF OF PREGNANCY.

-!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.

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-----

EMBL: M14647; AAA39947.1; -

DR EMBL: M85066; AAA75165.1; -

DR EMBL: M85062; AAA75165.1; JOINED.

DR EMBL: M85063; AAA75165.1; JOINED.

DR EMBL: M85064; AAA75165.1; JOINED.

DR PIR: A26489; A26489.

DR PIR: A44090; A44090.

DR HSSP: Q28632; LAN3.

DR MGD: MGI:97607; P12.

DR InterPro: IPR001400; -

DR Pfam: PF00103; hormone; 1.

DR PRINTS: PR00836; SOMATOTROPIN.

DR PROSITE: PS00266; SOMATOTROPIN\_1; 1.

DR PROSITE: PS00338; SOMATOTROPIN\_2; 1.

KW Hormone; Placenta; Signal.

FT SIGNAL 1 31

FT CHAIN 32 222 PLACENTAL LACTOGEN II.

FT DISULFID 82 197 BY SIMILARITY.

FT DISULFID 214 222 BY SIMILARITY.

FT CONFLICT 101 160 MISSING (IN REF. 2).

SQ SEQUENCE 222 AA; 25159 MW; 5A0D19D03D76EB05 CRC64;

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Query Match 96.8%; Score 30; DB 1; Length 222;

Best Local Similarity 80.0%; Pred No. 1;le02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5

DB 173 WSAWS 177

-----

RESULT 12

GMCR\_HUMAN

ID GMCR\_HUMAN STANDARD; PRT; 400 AA.

AC P15509; Q14429; Q14430; Q14431; Q00207; Q16564;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR RECEPTOR ALPHA

DE CHAIN PRECURSOR (GM-CSF-R-ALPHA) (GMR) (CDW116) (CD116 ANTIGEN).

GN CSF2RA OR CSF2R.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

KC TISSUE=Placenta;

RX MEDLINE=90059966; PubMed=2555171;

RA Gearing D.P., King J.A., Gough N.M., Nicola N.A.;

RT "Expression cloning of a receptor for human granulocyte-macrophage colony-stimulating factor.";

RL EMBO J. 8:3667-3676(1989).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=94193800; PubMed=8144676;

RA Nakagawa Y., Kosugi H., Miyajima A., Arai K.I., Yokota T.;

RT "Structure of the gene encoding the alpha subunit of the human granulocyte-macrophage colony stimulating factor receptor. Implications for the evolution of the cytokine receptor superfamily.";

RT J. Biol. Chem. 269:10905-10912(1994).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RX MEDLINE=91352066; PubMed=1715577;

RA Crosier K.E., Wong G.G., Mathey-Prevot B., Nathan D.G., Sieff C.A.;

RT "A functional isoform of the human granulocyte/macrophage colony-stimulating factor receptor has an unusual cytoplasmic domain.";

RT Proc. Natl. Acad. Sci. U.S.A. 88:7744-7748(1991).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 3).

RX TISSUE=Placenta;

RX MEDLINE=91088339; PubMed=2148207;

RA Ashworth A., Kraft A.;

RT "Cloning of a potentially soluble receptor for human GM-CSF.";

RL Nucleic Acids Res. 18:7178-7178(1990).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 3).

RX MEDLINE=91376112; PubMed=1832774;

RA Raines M.A., Liu L., Quan S.G., Joe V., DiPersio J.F., Golde D.W.;

RT "Identification and molecular cloning of a soluble human granulocyte-macrophage colony-stimulating factor receptor.";

RT Proc. Natl. Acad. Sci. U.S.A. 88:8203-8207(1991).

RN [6]

RP SEQUENCE FROM N.A. (ISOFORMS 4 AND 5).

RX TISSUE=Blood;

RX MEDLINE=94368898; PubMed=8086503;

RA Hu X., Emanuel P.D., Zuckerman K.S.;

RT "Cloning and sequencing of the cDNA encoding two alternative splicing-derived variants of the alpha subunit of the granulocyte-macrophage colony-stimulating factor receptor.";

RL Biochim. Biophys. Acta 1223:306-308(1994).

RN [7]

RP SEQUENCE FROM N.A. (ISOFORM 6).

RA Hu X., Zuckerman K.S.;

RT "Cloning and sequencing of the cDNA variant with 397 bp missing for the GM-CSF receptor alpha subunit.";

RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: LOW AFFINITY RECEPTOR FOR GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR. TRANSDUCES A SIGNAL THAT RESULTS IN THE PROLIFERATION, DIFFERENTIATION, AND FUNCTIONAL ACTIVATION OF HEMATOPOIETIC CELLS.

CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ISOFORMS 3, 4 AND 6 ARE PROBABLY SOLUBLE.

CC -!- ALTERNATIVE PRODUCTS: 6 ISOFORMS: 1 (SHOWN HERE), 2, 3, 4, 5 AND 6; ARE PRODUCED BY ALTERNATIVE SPLICING

CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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EMBL: X17648; CAA35638.1; -

DR EMBL: D26628; BAA05656.1; -

DR EMBL: D26618; BAA05656.1; JOINED.

DR EMBL: D26619; BAA05656.1; JOINED.

DR EMBL: D26620; BAA05656.1; JOINED.

DR EMBL: D26621; BAA05656.1; JOINED.

DR EMBL: D26622; BAA05656.1; JOINED.

DR EMBL: D26623; BAA05656.1; JOINED.

DR EMBL: D26624; BAA05656.1; JOINED.

DR EMBL: D26625; BAA05656.1; JOINED.

DR EMBL: D26626; BAA05656.1; JOINED.

DR EMBL: D26627; BAA05656.1; JOINED.

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QY 1 WSXWS 5
DB 77 WSAWS 81

RESULT 9
CRBB_MOUSE
ID CRBB_MOUSE STANDARD; PRT; 196 AA.
AC Q9JUV1;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE BETA CRYSTALLIN A2 (BETA-A2-CRYSTALLIN).
GN CRYBA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP
RC STRAIN=JMP4505;
RX MEDLINE=89013885; PubMed=2845223;
RA Walker M.J., Birch R.G., Pemberton J.M.;
RT "Cloning and characterization of an albicidin resistance gene from
RT Klebsiella oxytoca.";
RL Mol. Microbiol. 2:443-454(1988).
CC -!- FUNCTION: ALBICIDIN RESISTANCE PROTEIN BINDS TO FORM A COMPLEX
CC WITHOUT ANTIBIOTIC ACTIVITY BUT WITHOUT CATALYZING ANY FURTHER
CC CHEMICAL MODIFICATIONS TO ALBICIDIN.
CC -!- SUBCELLULAR LOCATION: PERIPLASMIC.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; Y00558; CAA68640.1;
CC PIR; S02828; S02828.
CC Antibiotic resistance; Periplasmic.
CC
CC SEQUENCE 218 AA; 25858 MW; 56578223BEDBCA7 CRC64;
SQ
Query Match 96.8%; Score 30; DB 1; Length 218;
Best Local Similarity 80.0%; Pred. No. 1:1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WSXWS 5
DB 57 WSAWS 61

RESULT 11
PLC2_MOUSE
ID PLC2_MOUSE STANDARD; PRT; 222 AA.
AC P09586;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PLACENTAL LACTOGEN II PRECURSOR (PL-II).
GN PL2 OR PL-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP
RX MEDLINE=87041482; PubMed=3464966;
RA Jackson L.L., Colosi P., Talamantes F., Linzer D.I.H.;
RT "Molecular cloning of mouse placental lactogen cDNA.";
RT Proc. Natl. Acad. Sci. U.S.A. 83:8496-8500(1986).
[2]
RN SEQUENCE FROM N.A.
RP
RX MEDLINE=92237269; PubMed=1570305;
RA Shida M.M., Jackson-Grusby L.L., Ross S.R., Linzer D.I.H.;
RT "Placental-specific expression from the mouse placental lactogen II
RT gene promoter.";
RT Proc. Natl. Acad. Sci. U.S.A. 89:3864-3868(1992).
[3]
RN SEQUENCE OF 32-50.
RX MEDLINE=85242883; PubMed=3859888;
RA Linzer D.I.H., Lee S.-J., Orgren L., Talamantes F., Nathans D.;
RT "Identification of proliferin mRNA and protein in mouse placenta.";
RT
```

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RESULT 7
CRBB_BOVIN
ID CRBB_BOVIN STANDARD; PRT; 196 AA.
AC P26444.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BETA CRYSTALLIN A2 (BETA-A2-CRYSTALLIN).
GN CRYBA2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens;
RX MEDLINE=91340151; PubMed=1874445;
RA van Rens G.L., Driessen H.P.C., Nalini V., Slingsby C., de Jong W.W.,
RT "Isolation and characterization of cDNAs encoding beta A2- and beta
RT A4-crystallins: heterologous interactions in the predicted beta
RT A4-beta B2 heterodimer."
RL Gene 102:179-188(1991).
RN [2]
RP SEQUENCE OF 133-196.
RC TISSUE=Lens cortex;
RX MEDLINE=84132067; PubMed=6698025;
RA Berbers G.A.M., Hoekman W.A., Bloemendal H., de Jong W.W.,
RA Kleinschmidt T., Braunlitzer G.;
RT "Homology between the primary structures of the major bovine beta-
RT crystallin chains."
RL Eur. J. Biochem. 139:467-479(1984).
CC -!- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
CC OF THE VERTEBRATE EYE LENS.
CC -!- SUBUNIT: HOMO/HETERODIMER, OR COMPLEXES OF HIGHER ORDER. THE
CC STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED
CC THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS (BY SIMILARITY).
CC -!- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
CC VERY SIMILAR GREEK KEY MOTIFS.
CC -!- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
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CC -----
DR EMBL; M60329; AAA30402.1; -.
DR PIR; D27898.
DR PIR; JH0602; JH0602.
DR HSP; P02522; IBLB.
DR InterPro; IPR001064; -.
DR Pfam; PF00030; Crystall; 2.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 3.
KW Eye lens protein; Duplication.
FT INIT_MET 0 0 BY SIMILARITY.
FT DOMAIN 1 10 N-TERMINAL ARM.
FT DOMAIN 11 51 MOTIF 1.
FT DOMAIN 52 99 MOTIF 2.
FT DOMAIN 100 104 CONNECTING PEPTIDE.
FT DOMAIN 105 146 MOTIF 3.
FT DOMAIN 147 196 MOTIF 4.
FT CONFLICT 182 184 QAH -> HAQ (IN REF. 2).
SQ SEQUENCE 196 AA; 22099 MW; B694586F8903B47F CRC64;

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Query Match 96.8%; Score 30; DB 1; Length 196;  
 Best Local Similarity 80.0%; Pred. No. 97;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 WSXWS 5
DB 77 WSAWS 81

RESULT 8
CRBB_HUMAN
ID CRBB_HUMAN STANDARD; PRT; 196 AA.
AC P53672; O9Y562;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BETA CRYSTALLIN A2 (BETA-A2-CRYSTALLIN).
GN CRYBA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wistow G.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 108-141 AND 157-184 FROM N.A.
RX MEDLINE=96039268; PubMed=7490092;
RA Hulsebos T.J.M., Cerosaletti K.M., Fournier R.E.K., Sinke R.J.,
RA Rocchi M., Marzella R., Jenkins N.A., Gilbert N.C., Copeland N.G.;
RT "Identification of the human beta A2 crystallin gene (CRYBA2):
RT localization of the gene on human chromosome 2 and of the homologous
RT gene on mouse chromosome 1."
RL Genomics 28:543-548(1995).
CC -!- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
CC OF THE VERTEBRATE EYE LENS.
CC -!- SUBUNIT: HOMO/HETERODIMER, OR COMPLEXES OF HIGHER ORDER. THE
CC STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED
CC THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS (BY SIMILARITY).
CC -!- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
CC VERY SIMILAR GREEK KEY MOTIFS.
CC -!- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
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CC -----
DR EMBL; AF166331; AAD45388.1; -.
DR EMBL; X86395; CAA60147.1; -.
DR EMBL; X86396; CAA60148.1; -.
DR HSP; P02522; IBLB.
DR MIM; 600836; -.
DR InterPro; IPR001064; -.
DR Pfam; PF00030; Crystall; 2.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 3.
KW Eye lens protein; Duplication.
FT INIT_MET 0 0 BY SIMILARITY.
FT DOMAIN 1 10 N-TERMINAL ARM.
FT DOMAIN 11 51 MOTIF 1.
FT DOMAIN 52 99 MOTIF 2.
FT DOMAIN 100 104 CONNECTING PEPTIDE.
FT DOMAIN 105 146 MOTIF 3.
FT DOMAIN 147 196 MOTIF 4.
FT CONFLICT 116 116 Q -> L (IN REF. 2).
SQ SEQUENCE 196 AA; 21964 MW; F92FEE924844DF51 CRC64;

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Query Match 96.8%; Score 30; DB 1; Length 196;  
 Best Local Similarity 80.0%; Pred. No. 97;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Beriman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,  
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.-H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RA "The genome sequence of *Drosophila melanogaster*,"  
 RA Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE OF 62-142 FROM N.A.  
 RC STRAIN-CANTON-S;  
 RX MEDLINE=94211204; PubMed=8159165;  
 RA Daffre S., Kysten P., Samakovlis C., Hultmark D.,  
 RT "The lysozyme locus in *Drosophila melanogaster*: an expanded gene  
 RT family adapted for expression in the digestive tract.";  
 RL Mol. Gen. Genet. 242:152-162(1994).  
 CC -1- FUNCTION: UNLIKELY TO PLAY AN ACTIVE ROLE IN THE HUMORAL IMMUNE  
 CC DEFENSE. MAY HAVE A FUNCTION IN THE DIGESTION OF BACTERIA IN THE  
 CC FOOD. MAY BE INVOLVED IN THE CLEARANCE OF BACTERIA FROM THE LARVAL  
 CC GUT BEFORE METAMORPHOSIS.  
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES BETWEEN  
 CC N-ACETYL-D-GLUCOSAMINE AND N-ACETYL-MURAMIC ACID IN PEPTIDOGLYCAN  
 CC HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.  
 CC -1- TISSUE SPECIFICITY: FOUND IN THE MIDGUT.  
 CC -1- DEVELOPMENTAL STAGE: RISES DRAMATICALLY IN THE LATE THIRD INSTAR,  
 CC THEN DECREASES GRADUALLY DURING THE PUPAL STAGES. LOW EXPRESSION  
 CC IS FOUND IN ADULTS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AE003470; AAF47445.1;  
 CC EMBL: Z22224; CAA80226.1;  
 CC PIR: S32650; S32650.  
 CC HSP: P00698; IAT6.  
 CC FlyBase: FBgn004431; Lysx.  
 CC InterPro: IPR001916;  
 CC Pfam: PF00062; lys; 1.  
 CC PROSITE: PS00128; LACTALBUMIN\_LYSOZYME; 1.  
 KW Hydrolase; Glycosidase; Bacteriolytic enzyme; Signal;  
 KW Multigene family.

FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 142 LYSOZYME X.  
 FT DISULFID 25 140 BY SIMILARITY.  
 FT DISULFID 46 130 BY SIMILARITY.  
 FT DISULFID 81 97 BY SIMILARITY.  
 FT DISULFID 93 111 BY SIMILARITY.  
 FT ACT\_SITE 51 51 BY SIMILARITY.  
 FT ACT\_SITE 69 69 BY SIMILARITY.  
 FT CONFLICT 78 78 M -> L (IN REF. 2).  
 SQ SEQUENCE 142 AA; 15591 MW; 2A48035364B995BQ CRC64;  
 Query Match 96.8%; Score 30; DB 1; Length 142;  
 Best Local Similarity 80.0%; Pred. No. 73;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 WSXWS 5  
 DB 121 WSAWS 125  
 ID MPL\_MPLV STANDARD; PRT; 184 AA.  
 AC P40931;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE MYELOPROLIFERATIVE LEUKEMIA PROTEIN.  
 DE V-MPL.  
 GN Myeloproliferative leukemia virus (MPLV).  
 OS Viruses; Retroviridae.  
 OX NCBI\_TaxID=11973;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91084843; PubMed=2175677;  
 RA Souyri M., Vigon I., Penciolelli J.-F., Heard J.-M., Tambourin P.,  
 RA Wendling F.,  
 RT "A putative truncated cytokine receptor gene transduced by the  
 RT myeloproliferative leukemia virus immortalizes hematopoietic  
 RT progenitors.";  
 RL Cell 63:1137-1147(1990).  
 CC -1- FUNCTION: TRUNCATED FORM OF THE RECEPTOR FOR THROMBOPOIETIN.  
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A ENV-MPL  
 CC POLYPEPTIDE.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: M50350; AAA77654.1;  
 CC HSP: P19235; 1EBP.  
 CC PROSITE: PS01352; HEMATOPO\_REC\_L\_F1; PARTIAL.  
 CC InterPro: IPR000950;  
 CC InterPro: IPR002465;  
 CC Receptor; Transmembrane; Oncogene.  
 FT TRANSMEM 44 64 POTENTIAL.  
 SQ SEQUENCE 184 AA; 20558 MW; 7986D3363940B735 CRC64;  
 Query Match 96.8%; Score 30; DB 1; Length 184;  
 Best Local Similarity 80.0%; Pred. No. 92;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 WSXWS 5  
 DB 26 WSAWS 30

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QY 1 WSXWS 5
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Db 120 WSAWS 124

RESULT 4
LYSE_DROME
ID LYSE_DROME STANDARD: PRT: 140 AA.
AC P37159; Q9W0J5;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LYSE_DROME PRECURSOR (EC 3.2.1.17) (1,4-BETA-N-ACETYLURAMIDASE E).
GN LYSE OR CG1180.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RX MEDLINE=94211204; PubMed=8159165;
RA Daffre S., Kylisten P., Samakowis C., Hultmark D.;
RT "The lysozyme locus in Drosophila melanogaster: an expanded gene
RL family adapted for expression in the digestive tract.";
RN Mol. Gen. Genet. 242:152-162(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazew R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale M., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kimios I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: UNLIKELY TO PLAY AN ACTIVE ROLE IN THE HUMORAL IMMUNE
CC DEFENSE. MAY HAVE A FUNCTION IN THE DIGESTION OF BACTERIA IN THE
CC FOOD.
```

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CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES BETWEEN
CC N-ACETYL-D-GLUCOSAMINE AND N-ACETYLURAMIC ACID IN PEPTIDOGLYCAN
CC HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.
CC -!- TISSUE SPECIFICITY: FOUND IN THE MIDGUT.
CC -!- DEVELOPMENTAL STAGE: MAXIMAL EXPRESSION IS FOUND DURING THE THIRD
CC LARVAL INSTAR, IT DROPS TO BECOME UNDETECTABLE IN THE LATE PUPAL
CC STAGE. THE EXPRESSION IN ADULTS IS SIMILAR TO THAT OF FIRST AND
CC SECOND LARVAL INSTARS.
CC -!- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z22227; CAA80229.1; -.
CC DR EMBL; AE003470; AAF47451.1; -.
CC DR PIR; S32634; S32634.
CC DR HSSP; PL1941; LLMC.
CC DR PDBase; FB90004428; Lyse.
CC DR InterPro; IPR001916; -.
CC DR Pfam; PF00062; lys; 1.
CC DR PROSITE; PS00128; LACTALBUMIN_LYSOZYME; 1.
CC KW Hydrolase; Glycosidase; Bacteriolytic enzyme; Signal;
CC MW Multigene family.
CC FT SIGNAL 1 18 BY SIMILARITY.
CC FT CHAIN 19 140 LYSOZYME E.
CC FT DISULFID 24 139 BY SIMILARITY.
CC FT DISULFID 45 129 BY SIMILARITY.
CC FT DISULFID 80 96 BY SIMILARITY.
CC FT DISULFID 92 110 BY SIMILARITY.
CC FT ACT_SITE 50 50 BY SIMILARITY.
CC FT ACT_SITE 68 68 BY SIMILARITY.
CC FT CONFLICT 12 12 M -> L (IN REF. 1).
CC FT CONFLICT 76 76 N -> D (IN REF. 1).
CC FT CONFLICT 138 138 G -> D (IN REF. 1).
CC SQ SEQUENCE 140 AA; 15552 MW; CEB5465CF6B6F123 CRC64;

Query Match 96.8%; Score 30; DB 1; Length 140;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
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Db 120 WSAWS 124

RESULT 5
LYSE_DROME
ID LYSE_DROME STANDARD: PRT: 142 AA.
AC P37159; Q9W0J5;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LYSOZYME X PRECURSOR (EC 3.2.1.17) (1,4-BETA-N-ACETYLURAMIDASE X).
GN LYSE OR CG9120.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
```

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CC EMBL; 222225; CA80227.1; -  
 CC EMBL; AE003470; AAF47448.1; -  
 CC PIR; S32620; S32620.  
 CC PIR; S32643; S32643.  
 CC HSP; P11941; LLMC.  
 CC FlyBase; FBgn0004425; LysB.  
 CC InterPro; IPR000974; -  
 CC InterPro; IPR001916; -  
 CC Pfam; PF00062; Lys; 1.  
 CC PROSITE; PS00128; LACTALBUMIN\_LYSOZYME; 1.  
 CC Hydrolase; Glycosidase; Bacteriolytic enzyme; Signal;  
 KW Multigene family.  
 FT SIGNAL 1 18 BY SIMILARITY.  
 FT CHAIN 19 140 LYSOZYME B.  
 FT DISULFID 24 139 BY SIMILARITY.  
 FT DISULFID 45 129 BY SIMILARITY.  
 FT DISULFID 80 96 BY SIMILARITY.  
 FT DISULFID 92 110 BY SIMILARITY.  
 FT ACT\_SITE 50 50 BY SIMILARITY.  
 FT ACT\_SITE 68 68 BY SIMILARITY.  
 FT CONFLICT 12 13 LA -> SG (IN REF. 1).  
 FT SEQUENCE 140 AA; 15611 MW; 70AFA5321857F093 CRC64;

Query Match 96.8%; Score 30; DB 1; Length 140;

Best Local Similarity 80.0%; Pred. No. 73;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5

DB 120 WSAWS 124

# RESULT 3

LYSD\_DROME STANDARD; PRT; 140 AA.  
 AC P29614; Q9W0J6;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE LYSOZYME D PRECURSOR (EC 3.2.1.17) (1,4-BETA-N-ACETYLGLUCOSAMINASE D).  
 GN LYSD OR CG9118.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CANTON-S;  
 RC MEDLINE=92269751; PubMed=1589805;  
 RA Kysten P., Kimbrell D.A., Daffre S., Samakovlis C., Hultmark D.;  
 RT "The lysozyme locus in *Drosophila melanogaster*: different genes are expressed in midgut and salivary glands.";  
 RL Mol. Gen. Genet. 232:335-343(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY.  
 RC MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
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 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
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 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
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 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
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 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 CC -!- FUNCTION: UNLIKELY TO PLAY AN ACTIVE ROLE IN THE HUMORAL IMMUNE  
 CC DEFENSE. MAY HAVE A FUNCTION IN THE DIGESTION OF BACTERIA IN THE  
 CC FOOD.  
 CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES BETWEEN  
 CC N-ACETYL-D-GLUCOSAMINE AND N-ACETYLGLUCOSAMINE IN PEPTIDOLYCAN  
 CC HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.  
 CC -!- TISSUE SPECIFICITY: ANTERIOR SECTION OF THE MIDGUT.  
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED DURING ALL FEEDING STAGES OF  
 CC DEVELOPMENT IN BOTH LARVAE AND ADULT.  
 CC -!- INDUCTION: REPRESSED WHEN BACTERIA ARE INJECTED.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.  
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EMBL; X58382; CA441272.1; -  
 EMBL; AE003470; AAF47450.1; -  
 PIR; S20914; S20914.  
 HSP; P11941; LLMC.  
 FlyBase; FBgn0004427; LysD.  
 InterPro; IPR001916; -  
 Pfam; PF00062; Lys; 1.  
 PROSITE; PS00128; LACTALBUMIN\_LYSOZYME; 1.  
 Hydrolase; Glycosidase; Bacteriolytic enzyme; Signal;  
 KW Multigene family.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT CHAIN 19 140 LYSOZYME D.  
 FT DISULFID 24 139 BY SIMILARITY.  
 FT DISULFID 45 129 BY SIMILARITY.  
 FT DISULFID 80 96 BY SIMILARITY.  
 FT DISULFID 92 110 BY SIMILARITY.  
 FT ACT\_SITE 50 50 BY SIMILARITY.  
 FT ACT\_SITE 68 68 BY SIMILARITY.  
 FT SEQUENCE 140 AA; 15635 MW; 75C24CA6F85DF903 CRC64;

Query Match 96.8%; Score 30; DB 1; Length 140;

Best Local Similarity 80.0%; Pred. No. 73;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:  
RT "The genome sequence of *Drosophila melanogaster*."  
RL Science 287:2185-2195(2000).  
CC -!- FUNCTION: UNLIKELY TO PLAY AN ACTIVE ROLE IN THE HUMORAL IMMUNE  
CC DEFENSE. MAY HAVE A FUNCTION IN THE DIGESTION OF BACTERIA IN THE  
CC FOOD.  
CC  
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES BETWEEN  
CC N-ACETYL-D-GLUCOSAMINE AND N-ACETYL-MURAMIC ACID IN PEPTIDOGLYCAN  
CC HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.  
CC  
CC -!- TISSUE SPECIFICITY: FOUND IN THE MIDGUT.  
CC  
CC -!- DEVELOPMENTAL STAGE: MAXIMAL EXPRESSION IS FOUND DURING THE THIRD  
CC LARVAL INSTAR. IT DROPS TO BECOME UNDETECTABLE IN THE LATE PUPAL  
CC STAGE. THE EXPRESSION IN ADULTS IS SIMILAR TO THAT OF FIRST AND  
CC SECOND LARVAL INSTARS.  
CC  
CC -!- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.  
CC  
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CC  
CC -----  
CC EMBL; 222223; CA80225.1; -;  
CC EMBL; 222226; CA80228.1; -;  
CC EMBL; AE003470; AAF47449.1; ALT\_SEQ.  
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CC PIR; S32651; S32651.  
CC PIR; S32726; S32726.  
CC HSSP; P11941; ILWC.  
CC FlyBase; FBgn0011201; LysA.  
CC FlyBase; FBgn0004426; LysC.  
CC InterPro; IPR000974; -;  
CC InterPro; IPR001916; -;  
CC Pfam; PF00062; Lys; 1.  
CC PROSITE; PS00128; LACTALBUMIN\_LYSOZYME; 1.  
CC Hydrolase; Glycosidase; Bacteriolytic enzyme; Signal;  
CC Multigene family.  
CC SIGNAL 1 18 BY SIMILARITY.  
CC CHAIN 19 140 LYSOZYME A/C.  
CC DISULFID 24 139 BY SIMILARITY.  
CC DISULFID 45 129 BY SIMILARITY.  
CC DISULFID 80 96 BY SIMILARITY.  
CC DISULFID 92 110 BY SIMILARITY.  
CC ACT\_SITE 50 50 BY SIMILARITY.  
CC ACT\_SITE 68 68 BY SIMILARITY.  
CC CONFLICT 41 42 AR -> NK (IN REF. 1).  
CC SEQUENCE 140 AA; 15635 MW; 75C24CA6F85DF903 CRC64;  
  
CC Query Match 96.8%; Score 30; DB 1; Length 140;  
CC Best Local Similarity 80.0%; Pred. No. 73;  
CC Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
CC QY 1 WSXWS 5  
CC || ||  
CC Db 120 WSXWS 124  
  
CC RESULT 2  
CC LYSB\_DROME  
CC ID LYSB\_DROME STANDARD; PRT; 140 AA.  
CC AC Q08694; P37158; O9W0J8;  
CC DT 01-OCT-1994 (Rel. 30, Created)  
CC DT 01-OCT-2000 (Rel. 40, Last sequence update)  
CC DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE LYSOZYME B PRECURSOR (EC 3.2.1.17) (1,4-BETA-N-ACETYL-MURAMIDASE B).  
GN LYSB OR C01179.  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CANTON-S;  
RX MEDLINE=94211204; PubMed=8159165;  
RA Daffre S., Kysten P., Samakovlis C., Hultmark D.;  
RT "The lysozyme locus in *Drosophila melanogaster*: an expanded gene  
RT family adapted for expression in the digestive tract.";  
RL Mol. Gen. Genet. 242:152-162(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.C., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:  
RT "The genome sequence of *Drosophila melanogaster*."  
RL Science 287:2185-2195(2000).  
CC -!- FUNCTION: UNLIKELY TO PLAY AN ACTIVE ROLE IN THE HUMORAL IMMUNE  
CC DEFENSE. MAY HAVE A FUNCTION IN THE DIGESTION OF BACTERIA IN THE  
CC FOOD.  
CC  
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES BETWEEN  
CC N-ACETYL-D-GLUCOSAMINE AND N-ACETYL-MURAMIC ACID IN PEPTIDOGLYCAN  
CC HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.  
CC  
CC -!- TISSUE SPECIFICITY: FOUND IN THE MIDGUT.  
CC  
CC -!- DEVELOPMENTAL STAGE: MAXIMAL EXPRESSION IS FOUND DURING THE THIRD  
CC LARVAL INSTAR. IT DROPS TO BECOME UNDETECTABLE IN THE LATE PUPAL  
CC STAGE. THE EXPRESSION IN ADULTS IS SIMILAR TO THAT OF FIRST AND  
CC SECOND LARVAL INSTARS.  
CC  
CC -!- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC  
CC -----  
CC EMBL; 222223; CA80225.1; -;  
CC EMBL; 222226; CA80228.1; -;  
CC EMBL; AE003470; AAF47449.1; ALT\_SEQ.  
CC EMBL; AE003470; -; NOT\_ANNOTATED\_CDS.  
CC PIR; S32651; S32651.  
CC PIR; S32726; S32726.  
CC HSSP; P11941; ILWC.  
CC FlyBase; FBgn0011201; LysA.  
CC FlyBase; FBgn0004426; LysC.  
CC InterPro; IPR000974; -;  
CC InterPro; IPR001916; -;  
CC Pfam; PF00062; Lys; 1.  
CC PROSITE; PS00128; LACTALBUMIN\_LYSOZYME; 1.  
CC Hydrolase; Glycosidase; Bacteriolytic enzyme; Signal;  
CC Multigene family.  
CC SIGNAL 1 18 BY SIMILARITY.  
CC CHAIN 19 140 LYSOZYME A/C.  
CC DISULFID 24 139 BY SIMILARITY.  
CC DISULFID 45 129 BY SIMILARITY.  
CC DISULFID 80 96 BY SIMILARITY.  
CC DISULFID 92 110 BY SIMILARITY.  
CC ACT\_SITE 50 50 BY SIMILARITY.  
CC ACT\_SITE 68 68 BY SIMILARITY.  
CC CONFLICT 41 42 AR -> NK (IN REF. 1).  
CC SEQUENCE 140 AA; 15635 MW; 75C24CA6F85DF903 CRC64;  
  
CC Query Match 96.8%; Score 30; DB 1; Length 140;  
CC Best Local Similarity 80.0%; Pred. No. 73;  
CC Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
CC QY 1 WSXWS 5  
CC || ||  
CC Db 120 WSXWS 124  
  
CC RESULT 2  
CC LYSB\_DROME  
CC ID LYSB\_DROME STANDARD; PRT; 140 AA.  
CC AC Q08694; P37158; O9W0J8;  
CC DT 01-OCT-1994 (Rel. 30, Created)  
CC DT 01-OCT-2000 (Rel. 40, Last sequence update)  
CC DT 01-OCT-2000 (Rel. 40, Last annotation update)



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OM protein - protein search, using sw model

Run on: August 24, 2001, 17:31:52 ; Search time 15.19 Seconds  
(without alignments)

11.276 Million cell updates/sec

Title: US-09-532-263-1

Perfect score: 31

Sequence: 1 WSXWS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	ID	Description
1	30	96.8	1	LYSA_DROME
2	30	96.8	1	LYSB_DROME
3	30	96.8	1	LYSD_DROME
4	30	96.8	1	LYSE_DROME
5	30	96.8	1	LYSX_DROME
6	30	96.8	1	MPL_MPLV
7	30	96.8	1	CRBB_BOVIN
8	30	96.8	1	CRBB_HUMAN
9	30	96.8	1	CRBB_MOUSE
10	30	96.8	1	ALBR_KLEOX
11	30	96.8	222	PLC2_MOUSE
12	30	96.8	400	GMCR_HUMAN
13	30	96.8	437	ERR1_YEAST
14	30	96.8	437	PROP_MOUSE
15	30	96.8	494	ADRO_MOUSE
16	30	96.8	507	EPOR_MOUSE
17	30	96.8	507	EPOR_RAT
18	30	96.8	508	EPOR_HUMAN
19	30	96.8	584	COB_HUMAN
20	30	96.8	586	COB_FUGRO
21	30	96.8	595	SNX9_HUMAN
22	30	96.8	622	PLR1_HUMAN
23	30	96.8	625	TPOR_MOUSE
24	30	96.8	635	TPOR_HUMAN
25	30	96.8	843	CO7_HUMAN
26	30	96.8	867	SSPO_BOVIN
27	30	96.8	934	COB_HUMAN
28	30	96.8	972	CTAL_BACCI
29	30	96.8	997	AT57_HUMAN
30	30	96.8	1077	SM5A_MOUSE
31	30	96.8	1522	BAT3_HUMAN
32	30	96.8	1584	BAT1_HUMAN
33	29	93.5	1	TKN1_RABIT

## RESULT 1

ID	LYSA_DROME	STANDARD;	PRT;	140 AA.
AC	P37157; Q9W0J7;			
DT	01-OCT-1994 (Rel. 30, Created)			
DT	01-OCT-2000 (Rel. 40, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	LYSOZYME A/C PRECURSOR (EC 3.2.1.17) (1,4-BETA-N-ACETYL-MURAMIDASE A/C).			
GN	LYSA AND (LYSC OR CG9111).			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CANTON-S;			
RX	MEDLINE=94211204; PubMed=8159165;			
RA	Daffre S., Kylisten P., Samakovlis C., Hultmark D.;			
RT	"The lysozyme locus in Drosophila melanogaster: an expanded gene family adapted for expression in the digestive tract."			
RL	Mol. Gen. Genet. 242:152-162(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY;			
RX	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abriel J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,			
RA	Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,			
RA	Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,			
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,			
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,			
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,			
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,			
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,			
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,			
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,			

## ALIGNMENTS



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076510 PRELIMINARY; PRT; 238 AA.  
 ID 076510  
 AC 076510;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE THROMBOSPONDIN-RELATED ADHESIVE PROTEIN (FRAGMENT)  
 GN TRAP-C3.  
 OS Cryptosporidium parvum.  
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida;  
 OC Cryptosporidiidae; Cryptosporidium.  
 OX NCBI\_TaxID=5807;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MOREDUN;  
 RA Spano F., Putignani L., Crisanti A.;  
 RT "Identification of a Cryptosporidium parvum putative adhesive  
 RT molecule.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF073838; AAC26812.1; -;  
 DR InterPro; IPR000884; -;  
 DR InterPro; IPR002086; -;  
 DR Pfam; PF00090; tsp\_1; 2.  
 DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; UNKNOWN\_1.  
 DR SMART; SM00209; TSP1; 1.  
 FT NON\_TER 1  
 FT NON\_TER 238  
 SQ SEQUENCE 238 AA; 26307 MW; 28242DB88F62C5A2 CRC64;

Query Match 96.8%; Score 30; DB 5; Length 238;  
 Best Local Similarity 80.0%; Pred. NO. 4e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5  
 DB 47 WSSWS 51

## RESULT 15

Q19092 PRELIMINARY; PRT; 254 AA.  
 ID Q19092  
 AC Q19092;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE SIMILAR TO THROMBOSPONDIN.  
 GN F01F1.13.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,  
 RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,  
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstein L., Wilkinson-Sproat J., Wohlman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans.";  
 RL Nature 368:32-38(1994).  
 RN [2]  
 RP \*SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Miller N.;

RL Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; U13070; AAC46484.1; -;  
 DR InterPro; IPR000884; -;  
 DR Pfam; PF00090; tsp\_1; 2.  
 DR SMART; SM00209; TSP1; 1.  
 SQ SEQUENCE 254 AA; 29602 MW; F2DD714CDA62D9D6 CRC64;

Query Match 96.8%; Score 30; DB 5; Length 254;  
 Best Local Similarity 80.0%; Pred. NO. 4.2e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5  
 DB 58 WSTWS 62

Search completed: August 24, 2001, 17:34:11  
 Job time: 154 sec

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RA Fuh G., Wells J.A.;
RT "Prolactin receptor antagonists that inhibit the growth of breast
RL J. Biol. Chem. 270:13133-13137(1995).
DR EMBL: S78505; AAB34470.1; -.
DR HSSP: P16471; IEP3.
DR InterPro: IPR001777; -.
DR InterPro: IPR002996; -.
DR InterPro: IPR003528; -.
DR Pfam: PF00041; fn3; 2.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
FT NON_TER 1
SQ SEQUENCE 206 AA; 23950 MW; CED939781B3C804E CRC64;

Query Match 96.8%; Score 30; DB 4; Length 206;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 191 WSAWS 195

RESULT 11
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ID Q27950 PRELIMINARY; PRT; 229 AA.
AC Q27950;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE ERYTHROPOIETIN RECEPTOR (FRAGMENT).
GN EPOR.
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9915;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Suliman H.B., Feldman B., F Majiwa P.A.O., Logan-Henfrey L.L.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U61398; AAB03870.1; -.
DR HSSP: P19235; IEB4.
DR InterPro: IPR001777; -.
DR InterPro: IPR002996; -.
DR InterPro: IPR003528; -.
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
FT NON_TER 1
SQ SEQUENCE 229 AA; 25196 MW; F6E01C4AB07893E8 CRC64;

Query Match 96.8%; Score 30; DB 6; Length 229;
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Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 175 WSAWS 179

RESULT 12
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ID Q28206 PRELIMINARY; PRT; 229 AA.
AC Q28206;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)

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DE ERYTHROPOIETIN RECEPTOR (FRAGMENT).
GN EPOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Suliman H.B., Feldman B., F Majiwa P.A.O., Logan-Henfrey L.L.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U61399; AAB03871.1; -.
DR HSSP: P19235; IEB4.
DR InterPro: IPR001777; -.
DR InterPro: IPR002996; -.
DR InterPro: IPR003528; -.
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
FT NON_TER 1
SQ SEQUENCE 229 AA; 25170 MW; EDFAA6F110D992E2 CRC64;

Query Match 96.8%; Score 30; DB 6; Length 229;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 175 WSAWS 179

RESULT 13
Q97888
ID Q97888 PRELIMINARY; PRT; 234 AA.
AC Q97888;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE INTERLEUKIN-4 RECEPTOR ALPHA CHAIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Trigona W.T., Estes D.M.;
RT "Cloning of bovine homolog to interleukin-4 receptor alpha chain.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF081273; AAD16011.1; -.
DR InterPro: IPR001777; -.
DR InterPro: IPR002996; -.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 234 AA; 26722 MW; B068385D2C86EE1B CRC64;

Query Match 96.8%; Score 30; DB 6; Length 234;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 183 WSAWS 187

RESULT 14

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RX  NCBI_TaxID=5807;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=20389602; PubMed=10930736;
RA  Pedraza-Diaz S., Amar C., McLauchlin J.;
RT  "The identification and characterisation of an unusual genotype of
RT  Cryptosporidium from human faeces as Cryptosporidium meleagridis.";
RL  FEMS Microbiol. Lett. 189:189-194(2000).
DR  EMBL: AF248744; AAG01093.1; -.
FT  NON_TER 1
FT  NON_TER 168
SQ  SEQUENCE 168 AA; 18614 MW; F2AD32849A8B5E9C CRC64;

Query Match          96.8%; Score 30; DB 5; Length 168;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 WSXWS 5
DB  143 WSSWS 147

RESULT 7
Q9GZ22
ID  Q9GZ22 PRELIMINARY; PRT; 168 AA.
AC  Q9GZ22;
DT  01-MAR-2001 (TREMBLrel. 16, Created)
DT  01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT  01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE  THROMBOSPONDIN-RELATED ADHESIVE PROTEIN (FRAGMENT).
GN  TRAP-C1.
OS  Cryptosporidium parvum.
OC  Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC  Cryptosporidiidae; Cryptosporidium.
OX  NCBI_TaxID=5807;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=20389602; PubMed=10930736;
RA  Pedraza-Diaz S., Amar C., McLauchlin J.;
RT  "The identification and characterisation of an unusual genotype of
RT  Cryptosporidium from human faeces as Cryptosporidium meleagridis.";
RL  FEMS Microbiol. Lett. 189:189-194(2000).
DR  EMBL: AF248744; AAG01093.1; -.
FT  NON_TER 1
FT  NON_TER 168
SQ  SEQUENCE 168 AA; 18698 MW; 2D02BC437C2AA44D CRC64;

Query Match          96.8%; Score 30; DB 5; Length 168;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 WSXWS 5
DB  143 WSSWS 147

RESULT 8
Q9GZ21
ID  Q9GZ21 PRELIMINARY; PRT; 168 AA.
AC  Q9GZ21;
DT  01-MAR-2001 (TREMBLrel. 16, Created)
DT  01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT  01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE  THROMBOSPONDIN-RELATED ADHESIVE PROTEIN (FRAGMENT).
GN  TRAP-C1.
OS  Cryptosporidium meleagridis.
OC  Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC  Cryptosporidiidae; Cryptosporidium.
OX  NCBI_TaxID=93969;
RN  [1]
RP  SEQUENCE FROM N.A.

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RX  MEDLINE=20389602; PubMed=10930736;
RA  Pedraza-Diaz S., Amar C., McLauchlin J.;
RT  "The identification and characterisation of an unusual genotype of
RT  Cryptosporidium from human faeces as Cryptosporidium meleagridis.";
RL  FEMS Microbiol. Lett. 189:189-194(2000).
DR  EMBL: AF248744; AAG01093.1; -.
FT  NON_TER 1
FT  NON_TER 168
SQ  SEQUENCE 168 AA; 18576 MW; CE9516EE86479C3 CRC64;

Query Match          96.8%; Score 30; DB 5; Length 168;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 WSXWS 5
DB  143 WSSWS 147

RESULT 9
Q65971
ID  Q65971 PRELIMINARY; PRT; 191 AA.
AC  Q65971;
DT  01-NOV-1996 (TREMBLrel. 01, Created)
DT  01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT  01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE  HYPOTHETICAL 21.2 KDA PROTEIN.
OS  cucurbit aphid-borne yellows virus.
OC  Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
OC  Luteovirus.
OX  NCBI_TaxID=91753;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=N;
RX  MEDLINE=94303150; PubMed=8030201;
RA  Guillely H., Wipf-Scheibel C., Richards K., Lecoq H., Jonard G.;
RT  "Nucleotide sequence of cucurbit aphid-borne yellows luteovirus.";
RL  Virology 202:1012-1017(1994).
DR  EMBL: X76931; CAA54253.1; -.
DR  InterPro; IPR000515; -.
DR  InterPro; IPR001964; -.
DR  Pfam; PF01659; Luteo_Vpg; 1.
DR  PRINTS; PR00912; LVIRUSORF5.
DR  PROSITE; PS00402; BPD_TRANSF_INN_MEMBR; UNKNOWN_1.
KW  Hypothetical protein.
SQ  SEQUENCE 191 AA; 21154 MW; E0C64CC99E555520 CRC64;

Query Match          96.8%; Score 30; DB 14; Length 191;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 WSXWS 5
DB  97 WSSWS 101

RESULT 10
Q16354
ID  Q16354 PRELIMINARY; PRT; 206 AA.
AC  Q16354;
DT  01-NOV-1996 (TREMBLrel. 01, Created)
DT  01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT  01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE  PROLACTIN RECEPTOR (FRAGMENT).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=95286597; PubMed=7768908;

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DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE TRAP-C1 (FRAGMENT).  
 GN TRAP-C1.  
 OS Cryptosporidium parvum.  
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
 CC Cryptosporidiidae; Cryptosporidium.  
 OX NCBI\_TaxID=5807;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-P12 (NATURAL ISOLATE);  
 RA Spano F., Putignani L., Guida S., Crisanti A.;  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF033829; AAB92610.1; -  
 DR InterPro; IPR000884; -  
 DR SMART; SM00209; TSP1; 1.  
 FT NON\_TER 1  
 FT NON\_TER 72  
 FT NON\_TER 72  
 SQ SEQUENCE 72 AA; 7564 MW; 7D2AED67148F1518 CRC64;

Query Match 96.8%; Score 30; DB 5; Length 72;  
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 WSXWS 5  
 DB 16 WSTWS 20

RESULT 3  
 ID Q9H2J5 PRELIMINARY; PRT; 97 AA.  
 AC Q9H2J5;  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE MITOGALIGIN.  
 GN GALIG.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Legrand A., Guittaut M., Charpentier S., Normand T., Dubois M.,  
 RA Rainond J.;  
 RT "Identification of an internal gene to the human Galectin-3 gene  
 RT encoding two novel proteins from different overlapping reading  
 RT frames.";  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF266280; AAG44702.1; -  
 SQ SEQUENCE 97 AA; 11168 MW; B9CF5CECAEA7C055 CRC64;

Query Match 96.8%; Score 30; DB 4; Length 97;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 WSXWS 5  
 DB 44 WSTWS 48

RESULT 4  
 ID Q61427 PRELIMINARY; PRT; 147 AA.  
 AC Q61427;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE PROCOLLAGEN, TYPE I, ALPHA 1 (ALPHA 1 TYPE I COLLAGEN) (FRAGMENT).  
 GN COL1A1 OR COL1A1.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=LIVER;  
 RX MEDLINE=94344105; PubMed=8065328;  
 RA Rhodes K., Rippe R.A., Umezawa A., Nehls M., Brenner D.A., Breindl M.;  
 RT "DNA methylation represses the murine alpha 1(I) collagen promoter by  
 RT an indirect mechanism";  
 RL Mol. Cell. Biol. 14:5950-5960(1994).  
 DR EMBL; X54876; CAA38657.1; -  
 DR MGD; MGI:88467; Col1a1.  
 DR InterPro; IPR001007; -  
 DR Pfam; PF00093; vwc; 1.  
 DR PROSITE; PS01208; VWFC; 1.  
 DR SMART; SM00214; VWC; 1.  
 FT NON\_TER 147  
 FT NON\_TER 147  
 SQ SEQUENCE 147 AA; 16652 MW; 9263BF0A91B4307D CRC64;

Query Match 96.8%; Score 30; DB 11; Length 147;  
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 WSXWS 5  
 DB 132 WSSWS 136

RESULT 5  
 ID Q38069 PRELIMINARY; PRT; 162 AA.  
 AC Q38069;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-JAN-1999 (TReMBLrel. 09, Last annotation update)  
 DE TAIL TUBE PROTEIN (GPFII).  
 GN FII.  
 OS Bacteriophage PSI7.  
 OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae.  
 OX NCBI\_TaxID=33710;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sasaki T., Shinomiya T., Kumazaki T., Mohri N., Ishii S., Arisaka F.;  
 RT "Nucleotide sequence of the contractile tail sheath and tube genes of  
 RT bacteriophage PSI7 and the amino acid sequence of the gene products.";  
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; D26449; BAA05468.1; -  
 SQ SEQUENCE 162 AA; 17688 MW; 8275079A1C2E8FE6 CRC64;

Query Match 96.8%; Score 30; DB 9; Length 162;  
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 WSXWS 5  
 DB 55 WSAWS 59

RESULT 6  
 ID Q9GZ23 PRELIMINARY; PRT; 168 AA.  
 AC Q9GZ23;  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE THROMBOSPONDIN-RELATED ADHESIVE PROTEIN (FRAGMENT).  
 GN TRAP-C1.  
 OS Cryptosporidium parvum.  
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
 CC Cryptosporidiidae; Cryptosporidium.

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 24, 2001, 17:31:37 ; Search time 37.87 Seconds  
(without alignments)  
17.468 Million cell updates/sec

Title: US-09-532-263-1  
Perfect score: 31  
Sequence: 1 WSXWS 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL16.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_unclassified.\*  
13: sp\_vertebrate.\*  
14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	96.8	52	Q16340	Q16340 homo sapien
2	30	96.8	72	O43983	O43983 cryptospori
3	30	96.8	97	Q942J5	Q9h215 homo sapien
4	30	96.8	147	O61427	O61427 mus musculu
5	30	96.8	162	Q38069	Q38069 bacterioph
6	30	96.8	168	Q9GZ23	Q9g223 cryptospori
7	30	96.8	168	Q9GZ22	Q9g222 cryptospori
8	30	96.8	168	Q9GZ21	Q9g221 cryptospori
9	30	96.8	191	Q65971	Q65971 cucurbit ap
10	30	96.8	206	Q16354	Q16354 homo sapien
11	30	96.8	229	Q27950	Q27950 bos indicus
12	30	96.8	229	Q28206	Q28206 bos taurus
13	30	96.8	234	Q97888	Q97888 bos taurus
14	30	96.8	238	O76510	O76510 cryptospori
15	30	96.8	254	O19092	Q19092 caenorhabdi
16	30	96.8	291	O20991	Q20991 caenorhabdi
17	30	96.8	294	O20991	Q20991 zymomonas m
18	30	96.8	304	O9RMF3	Q9rmf3 caenorhabdi
19	30	96.8	316	Q9XU51	Q9xu51 caenorhabdi
					O35545 rattus norv

20	30	96.8	328	4	O95061	O95061 homo sapien
21	30	96.8	332	14	Q82493	Q82493 influenza a
22	30	96.8	349	4	Q9UJH5	Q9ujh5 homo sapien
23	30	96.8	367	1	O59408	O59408 pyrococcus
24	30	96.8	375	9	Q92X59	Q92x59 mycobacteri
25	30	96.8	388	1	O9VIG1	O9vlg1 pyrococcus
26	30	96.8	394	2	O33205	O33205 mycobacteri
27	30	96.8	422	4	Q16542	Q16542 homo sapien
28	30	96.8	425	6	O02661	O02661 bos taurus
29	30	96.8	428	5	Q9VN52	Q9vn52 drosophila
30	30	96.8	432	11	P70225	P70225 mus musculu
31	30	96.8	432	11	O64385	O64385 mus musculu
32	30	96.8	437	3	Q12007	Q12007 saccharomyc
33	30	96.8	446	4	O43384	O43384 homo sapien
34	30	96.8	455	3	O08231	O08231 saccharomyc
35	30	96.8	509	6	Q9MYZ9	Q9myz9 sus scrofa
36	30	96.8	528	2	P70733	P70733 aeromonas c
37	30	96.8	558	5	O9V7B4	O9v7b4 drosophila
38	30	96.8	558	13	Q9PVW6	Q9pvw6 paralichthy
39	30	96.8	579	10	Q9STS3	Q9stv3 arabidopsis
40	30	96.8	588	13	Q9PVW7	Q9pvw7 paralichthy
41	30	96.8	612	8	Q9MQV2	Q9mqv2 trititum ae
42	30	96.8	622	6	Q9NCJ7	Q9ncj7 callithrix
43	30	96.8	633	4	Q9Y590	Q9y590 homo sapien
44	30	96.8	647	5	Q9U217	Q9u217 caenorhabdi
45	30	96.8	654	5	Q19284	Q19284 caenorhabdi

ALIGNMENTS

RESULT 1  
Q16340  
ID Q16340 PRELIMINARY; PRT; 52 AA.  
AC Q16340;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE PHOSPHODIESTERASE BETA-SUBUNIT PROTEIN (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95322980; PubMed=7599633;  
RA Bayes M., Giordano M., Balcells S., Grinberg D., Villageliu L.,  
RA Martinez I., Ayuso C., Benitez J., Ramos-Arroyo M.A., Chivelet P.,  
RA Et AL.;  
RT "Homozygous tandem duplication within the gene encoding the beta-  
RT subunit of rod phosphodiesterase as a cause for autosomal recessive  
RT retinitis pigmentosa";  
RL Hum. Mutat. 5:228-234(1995).  
DR EMBL; S78008; AADI4270.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 52 AA; 6124 MW; 4FC1A6A8C9DAEF94 CRC64;

Query Match 96.8%; Score 30; DB 4: Length 52;  
Best Local Similarity 80.0%; Pred. No. 99;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 WSXWS 5  
DB 42 WSXWS 46

RESULT 2  
O43983 PRELIMINARY; PRT; 72 AA.  
ID O43983  
AC O43983;  
DT 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)